


```
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 813
; LENGTH: 6439
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-813

Alignment Scores:
Pred. No.: 731 Length: 6439
Score: 49.50 Matches: 9
Percent Similarity: 69.23% Conservative: 9
Best Local Similarity: 34.62% Mismatches: 7
Query Match: 33.67% Indels: 1
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-902-540-813 (1-6439)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsn---ArgMetSer 21
Db 4083 GCTGGTATGGCCAGCAAGATTCCTCCAAACCCCAATGGATGGGACAAACGCCCAACTGCAC 4142
Qy 22 AlaMetIleProGluIle 27
Db 4143 GCGCTCATGAAGGATGTC 4160

RESULT 30
US-09-949-016-13465/c
; Sequence 13465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13465
; LENGTH: 27579
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13465

Alignment Scores:
Pred. No.: 4,89e+03 Length: 27579
Score: 49.50 Matches: 12
Percent Similarity: 38.46% Conservative: 3
Best Local Similarity: 30.77% Mismatches: 7
Query Match: 33.67% Indels: 17
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-949-016-13465 (1-27579)

Qy 5 LeuAlaLeuLeuTyrProThrAsnArg----- 13
Db 6046 ATACTATTATTATATACCCGTTTATAGATGAGAAACTGAGGCCCGAGATTAAAGTAATTG 5987
Qy 14 -----AsnLysTrpAspAsnArgMetSerAlaMetIleProGlu 26
Db 5986 CCCCAAGGTCACATAGCTGCAGACTGGGATTCAAACTCAAGCTCTCTCATTCAGAG 5930

RESULT 31
US-09-949-016-17490
; Sequence 17490, Application US/09949016
; Patent No. 6812339
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17490
; LENGTH: 141115
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(141115)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17490

Alignment Scores:
Pred. No.: 4,09e+04 Length: 141115
Score: 49.50 Matches: 10
Percent Similarity: 59.09% Conservative: 3
Best Local Similarity: 45.45% Mismatches: 2
Query Match: 33.67% Indels: 7
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-949-016-17490 (1-141115)

Qy 4 GlyLeuAlaLeuLeuTyrProThrAsnArg-----AsnLysTrp 16
Db 14577 GCCTTGACTCTTTTATTTCTTCTTAACAGATGAGCTGACATGGGCTATCAACACGGGTGG 14636
Qy 17 AspAsn 18
Db 14637 GAAAC 14642

RESULT 32
US-08-458-516-21
; Sequence 21, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
```

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/149,718
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/660,487
;; FILING DATE:
;; APPLICATION NUMBER: 08/480,653
;; FILING DATE: June 7, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabat, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: ANS101CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404)-873-8794
;; TELEFAX: (404)-873-8795
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2085 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1-2085
;; OTHER INFORMATION: /function= "coding region for APP695."
US-09-149-718-1

Alignment Scores:
Pred. No.: 138 Length: 2085
Score: 50.00 Matches: 11
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 40.74% Mismatches: 12
Query Match: 34.01% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-149-718-1 (1-2085)

QY 2 AlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMetSer 21
Db 1643 AGTTCGGGGCTGACTCTGTGCCAGCCCAACAGAAACGAAGTTGAGCCTGTTGATGCCC 1702
QY 22 AlaMetIleProGluIleAsp 28
Db 1703 GCCCTGCTGCCGACCGAGGAC 1723

RESULT 27
US-09-902-540-611
; Sequence 611, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 611
; LENGTH: 2388
; TYPE: DNA
; ORGANISM: Myxococcus xanthus

US-09-902-540-611
Alignment Scores:
Pred. No.: 164 Length: 2388
Score: 50.00 Matches: 11
Percent Similarity: 56.00% Conservative: 3
Best Local Similarity: 44.00% Mismatches: 11
Query Match: 34.01% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-902-540-611 (1-2388)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMet 20
Db 382 TCCAACTCGGCTTTCGGCTGTCTACCCCGCGCTCCAGTCTCTGGCCAGCCGCC 441
QY 21 SerAlaMetIlePro 25
Db 442 TCCGCCTGGAGACCC 456

RESULT 28

US-09-949-016-16923
; Sequence 16923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16923
; LENGTH: 390416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16923

Alignment Scores:
Pred. No.: 1.24e+05 Length: 390416
Score: 50.00 Matches: 8
Percent Similarity: 73.33% Conservative: 3
Best Local Similarity: 53.33% Mismatches: 4
Query Match: 34.01% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-949-016-16923 (1-390416)

QY 13 ArgAsnLysTyrAspAsnArgMetSerAlaMetIleProGluIle 27
Db 228116 AAAACAATGGCAGAGAAAGTTTCAGCTGTATTTCCAGAAATA 228160

RESULT 29
US-09-902-540-813
; Sequence 813, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4
OTHER INFORMATION: seq FSFLLGMGGCLP/GF
NAME/KEY: polyA site
LOCATION: 536..547
US-09-663-600A-137

Alignment Scores:
Pred. No.: 24 Length: 547
Score: 50.00 Matches: 12
Percent Similarity: 60.00% Conservative: 3
Best Local Similarity: 48.00% Mismatches: 6
Query Match: 34.01% Indels: 4
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-663-600A-137 (1-547)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 400 GCAGGCTCTGGGCTTTTCTCCTTATGTTACT-----TGAATGGCGGGTG 447

Qy 21 SerAlaMetIlePro 25

Db 448 CCTGCCTGGATTCCT 462

RESULT 24
US-09-663-600A-43
Sequence 43, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 43

LENGTH: 648
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 460..555
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4
OTHER INFORMATION: seq FSFLLGMGGCLP/GF
NAME/KEY: polyA signal
LOCATION: 614..619
NAME/KEY: polyA site
LOCATION: 635..648
US-09-663-600A-43

Alignment Scores:
Pred. No.: 29.9 Length: 648
Score: 50.00 Matches: 12
Percent Similarity: 60.00% Conservative: 3

Best Local Similarity: 48.00% Mismatches: 6
Query Match: 34.01% Indels: 4
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-663-600A-43 (1-648)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 501 GCAGGCTCTGGGCTTTTCTCCTTATGTTACT-----TGAATGGCGGGTG 548

Qy 21 SerAlaMetIlePro 25

Db 549 CCTGCCTGGATTCCT 563

RESULT 25
US-09-248-796A-738
Sequence 738, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 738
LENGTH: 1008
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-738

Alignment Scores:
Pred. No.: 53.2 Length: 1008
Score: 50.00 Matches: 12
Percent Similarity: 60.71% Conservative: 5
Best Local Similarity: 42.86% Mismatches: 2
Query Match: 34.01% Indels: 9
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-248-796A-738 (1-1008)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 559 AGTGGTATTGCTATAGTCTATACCAAGGATCGAAAAAAGTATTTTACAAACATTTTGTG 618

Qy 16 ----TrpAspAsnArgMetSer 21
Db 619 AATTGGGATTCCTCGGTTGAGT 640

RESULT 26
US-09-149-718-1
Sequence 1, Application US/09149718
Patent No. 6717031
GENERAL INFORMATION:
APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
APPLICANT: Peter A. Seubert, and Russell E. Rydel
TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
TITLE OF INVENTION: Therapeutics Using Transgenic Animal Models
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15820
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15820

Alignment Scores:
Pred. No.:          6.41e+03          53394
Score:              51.00             11
Percent Similarity: 65.22%             4
Best Local Similarity: 47.83%           8
Query Match:        34.69%             0
DB:                  4                0

US-10-014-101B-32 (1-28) x US-09-949-016-15820 (1-53394)

Qy      1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db      41543 AGTGCCTCTGGAGTGGCCGATCTGATGTGTCCACGCGTCCCTCCTGGAATCGGCGGATG 41484

Qy      21 SerAlaMet 32
Db      41483 GACGCGGTC 41475

RESULT 21
US-09-596-002-32/c
; Sequence 32, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 62909
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 32
; PUBLICATION INFORMATION:
US-09-596-002-32

Alignment Scores:
Pred. No.:          7.94e+03          62909
Score:              51.00             8
Percent Similarity: 76.47%             5
Best Local Similarity: 47.06%           4
Query Match:        34.69%             0
DB:                  4                0

US-10-014-101B-32 (1-28) x US-09-596-002-32 (1-62909)

Qy      1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAsp 17
Db      6032 TCTACACAGGCATATCCATAAAGTATCCTTAAATATCAATGAATGGAT 5982

RESULT 22
US-09-902-540-6994/c
```

```
; Sequence 6994, Application US/099025540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6994
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6994

Alignment Scores:
Pred. No.:          21.9              510
Score:              50.00             11
Percent Similarity: 56.00%             3
Best Local Similarity: 44.00%           11
Query Match:        34.01%             0
DB:                  4                0

US-10-014-101B-32 (1-28) x US-09-902-540-6994 (1-510)

Qy      1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db      131 TCCAACTCCGGCTTTCGGCTGTCTACCCAGCGCTCCAGTTCCTGGCCAGCCGCC 72

Qy      21 SerAlaMetIlePro 25
Db      71 TCCGCTGGAGACCC 57

RESULT 23
US-09-663-600A-137
; Sequence 137, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 137
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 359..454
```


; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15817
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15817

Alignment Scores:
Pred. No.: 6.41e+03 Length: 53394
Score: 51.00 Matches: 11
Percent Similarity: 65.22% Conservative: 4
Best Local Similarity: 47.83% Mismatches: 8
Query Match: 34.69% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-949-016-15817 (1-53394)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
|||||
Db 41543 AGTGCCTCTGGAGTGGCCGATCTGATGTTGTCCACGCGTCCCTCCTGGAATCGGCGGATG 41484
|||||

Qy 21 SerAlaMet 23
|||
Db 41483 GACGCGCTC 41475

RESULT 18
US-09-949-016-15818/c
; Sequence 15818, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15818
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15818

Alignment Scores:
Pred. No.: 6.41e+03 Length: 53394
Score: 51.00 Matches: 11
Percent Similarity: 65.22% Conservative: 4
Best Local Similarity: 47.83% Mismatches: 8
Query Match: 34.69% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-949-016-15818 (1-53394)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
|||||
Db 41543 AGTGCCTCTGGAGTGGCCGATCTGATGTTGTCCACGCGTCCCTCCTGGAATCGGCGGATG 41484
|||||
Qy 21 SerAlaMet 23
|||
Db 41483 GACGCGCTC 41475

RESULT 19
US-09-949-016-15819/c
; Sequence 15819, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15819
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15819

Alignment Scores:
Pred. No.: 6.41e+03 Length: 53394
Score: 51.00 Matches: 11
Percent Similarity: 65.22% Conservative: 4
Best Local Similarity: 47.83% Mismatches: 8
Query Match: 34.69% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-949-016-15819 (1-53394)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
|||||
Db 41543 AGTGCCTCTGGAGTGGCCGATCTGATGTTGTCCACGCGTCCCTCCTGGAATCGGCGGATG 41484
|||||
Qy 21 SerAlaMet 23
|||
Db 41483 GACGCGCTC 41475

RESULT 20
US-09-949-016-15820/c
; Sequence 15820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

STATE: Iowa
COUNTRY: USA
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,761A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 212-US
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5198 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-123-761A-1

Alignment Scores:
Pred. No.: 206 Length: 5198
Score: 52.00 Matches: 11
Percent Similarity: 66.67% Conservative: 5
Best Local Similarity: 45.83% Mismatches: 8
Query Match: 35.37% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-32 (1-28) x US-08-123-761A-1 (1-5198)

QY 1 SerAlaSerGlyLeuAlaLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 4527 ACCGCCTCCGCTCGACGAGATCAATCCACCAATCGCAACAGAAACGTAATCGGCAG 4468
QY 21 SerAlaMetile 24
Db 4467 TCAGTTCTTG 4456

RESULT 15
US-09-949-016-17547/c
; Sequence 17547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17547
; LENGTH: 84870
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(84870)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17547

Alignment Scores:
Pred. No.: 7.91e+03 Length: 84870
Score: 52.00 Matches: 11
Percent Similarity: 60.71% Conservative: 6
Best Local Similarity: 39.29% Mismatches: 11
Query Match: 35.37% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-949-016-17547 (1-84870)

QY 1 SerAlaSerGlyLeuAlaLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 4466 TCATTTACTAACTGGGCCTATTACATGTGTCAAACCTAATACAAATGGGAAATAGAAC 4407
QY 21 SerAlaMetileProGluileAsp 28
Db 4406 ACTAATTTCTTACCTTTTCATAGAC 4383

RESULT 16

US-09-657-252-3/c
; Sequence 3, Application US/09657252
; Patent No. 6500643
; GENERAL INFORMATION:
; APPLICANT: Wu, Dong-Hai
; APPLICANT: Gu, Yunrong
; APPLICANT: Millard, William
; APPLICANT: He, Yun-Je
; TITLE OF INVENTION: Human High Affinity Choline Transporter cDNA
; FILE REFERENCE: MBHB00-639
; CURRENT APPLICATION NUMBER: US/09/657,252
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1893)
US-09-657-252-3

Alignment Scores:
Pred. No.: 81.7 Length: 1893
Score: 51.00 Matches: 11
Percent Similarity: 65.22% Conservative: 4
Best Local Similarity: 47.83% Mismatches: 8
Query Match: 34.69% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-657-252-3 (1-1893)

QY 1 SerAlaSerGlyLeuAlaLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1379 AGTGCCTCTGGAGTGGCCGATCTGATGTTGTCCAGGCGTCCCTCTCGAATCGCGGATG 1320
QY 21 SerAlaMet 23
Db 1319 GACGCGTC 1311

RESULT 17

US-09-949-016-15817/c
; Sequence 15817, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

```
; Sequence 13046, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13046
; LENGTH: 28555
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(28555)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13046

Alignment Scores:
Pred. No.:      866      Length:      28555
Score:          54.00    Matches:      11
Percent Similarity: 56.52%  Conservative: 2
Best Local Similarity: 47.83%  Mismatches: 2
Query Match:      36.73%    Indels:      8
DB:              4         Gaps:       1

US-10-014-101B-32 (1-28) x US-09-949-016-13046 (1-28555)

Qy      3 SerGlyLeuAlaLeuLeu-----TyrProThrAsnArgAsn 14
      |||||::: |||||
Db      27369 TCTGGGATGCATTGTTGTCTTCAGAACCCCTTCTCCCATACCTGTGATATAAAAC 27310

Qy      15 LysTrpAsp 17
      |||||
Db      27309 AAATGGGAC 27301

RESULT 13
US-08-261-206A-71/c
; Sequence 71, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; WITH THROMBIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3306 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Acremonium chrysogenum
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..3306
; OTHER INFORMATION: /label= PGK gene
; OTHER INFORMATION: /note= "Nucleotide sequence of region A in Figure
; OTHER INFORMATION: 59. The sequence is presented as Figure 61."
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1252..1317
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1463..1883
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1948..2715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1252..1317, 1463..1883, 1948..2714)
US-08-261-206A-71

Alignment Scores:
Pred. No.:      63.1      Length:      3306
Score:          53.50    Matches:      13
Percent Similarity: 53.12%  Conservative: 4
Best Local Similarity: 40.62%  Mismatches: 8
Query Match:      36.39%    Indels:      7
DB:              1         Gaps:       1

US-10-014-101B-32 (1-28) x US-08-261-206A-71 (1-3306)

Qy      1 SerAlaSerGly-----LeuAlaLeuLeuTyrProThrAsnArg 13
      |||||::: |||||
Db      1653 TCGAGCTCGGGACGACGGGCTGCAGCGAGTACTTGGGGTTGGGGTGGCGGCGG 1594

Qy      14 AsnLysTrpAspAsnArgMetSerAlaMetIlePro 25
      ::|||::: |||||::: |||||
Db      1593 CCAAGGTGGGACATGAGGATGACGGCCTTGGCGCCA 1558

RESULT 14
US-08-123-761A-1/c
; Sequence 1, Application US/08123761A
; Patent No. 5589611
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Johal, Gurmukh S.
; TITLE OF INVENTION: A DISEASE RESISTANCE GENE FROM MAIZE AS
; TITLE OF INVENTION: A SELECTABLE MARKER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lactococcus cremoris
STRAIN: IL964
US-08-248-466B-2

Alignment Scores:
Pred. No.: 27.6 Length: 2763
Score: 55.00 Matches: 12
Percent Similarity: 58.33% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 10
Query Match: 37.41% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-32 (1-28) x US-08-248-466B-2 (1-2763)

QY 5 LeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIle 24
Db 540 TTAGCCCTCTTAATTCCTTAACTCGTCATAAAGTGATAAACGTTTTTCTGTAAGCCTG 481
QY~ 25 ProGluIleAsp 28
Db 480 CCATTATTGAC 469

RESULT 10
US-09-949-016-13407/c
Sequence 13407, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13407
LENGTH: 32616
TYPE: DNA
ORGANISM: Human
US-09-949-016-13407

Alignment Scores:
Pred. No.: 694 Length: 32616
Score: 55.00 Matches: 11
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 52.38% Mismatches: 7
Query Match: 37.41% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-949-016-13407 (1-32616)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 17874 TCACCTCAGGGCCTAGCAATCCTGGATGACACGTCTGAGACAAATGGGACAGAGGAA 17815

QY 21 Ser 21
Db 17814 AGT 17812
RESULT 11
US-09-023-655-543
Sequence 543, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: STOMNOT01
CLONE: 221877
US-09-023-655-543

Alignment Scores:
Pred. No.: 11.3 Length: 1031
Score: 54.00 Matches: 11
Percent Similarity: 56.52% Conservative: 2
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 36.73% Indels: 8
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-023-655-543 (1-1031)

QY 3 SerGlyLeuAlaLeuLeu-----TyrProThrAsnArgAsn 14
Db 281 TCTGGATGCATTGTTCCTTTTCAGAACCTTCCTCCCATACCTGTGATAAAAC 340
QY 15 LysTyrAsp 17
Db 341 AAATGGGAC 349

RESULT 12
US-09-949-016-13046/c

OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (207)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (210)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (213)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (216)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (219)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (225)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (228)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (231)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (234)
OTHER INFORMATION: a,g,c or t
NAME/KEY: variation
LOCATION: (237)
OTHER INFORMATION: a,g,c or t

Alignment Scores:

Pred. No.: 4.15 Length: 1602
Score: 58.00 Matches: 10
Percent Similarity: 56.00% Conservative: 4
Best Local Similarity: 40.00% Mismatches: 11
Query Match: 39.46% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-663-326-10 (1-1602)

QY 4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMetSerAlaMet 23
Db 1276 GGNCCNYTNATHGTNTAYCCNYTNAAYAAARWSNATGTGGGAYGAYGNATGWSNGCNGCN 1335
QY 24 IleProGluIleAsp 28
Db 1336 ACNCCNWSNGARGAY 1350

RESULT 5

US-09-949-016-62602
Sequence 62602, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 62602
LENGTH: 601
TYPE: DNA
ORGANISM: Human

US-09-949-016-62602

Alignment Scores:

Pred. No.: 3.09 Length: 601
Score: 55.50 Matches: 12
Percent Similarity: 63.64% Conservative: 2
Best Local Similarity: 54.55% Mismatches: 5
Query Match: 37.76% Indels: 3
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-949-016-62602 (1-601)

QY 7 LeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMetSer-----AlaMet 23
Db 299 TTTCATACAAAAGGAGAGGACAAATGGGACAATTGATGTACATACGGCTGCTATG 358
QY 24 IlePro 25
Db 359 GTCCCT 364

RESULT 6

US-09-949-016-12545/c
Sequence 12545, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12545
LENGTH: 163662
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(163662)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12545

Alignment Scores:

Pred. No.: 4.68e+03 Length: 163662
Score: 55.50 Matches: 12
Percent Similarity: 63.64% Conservative: 2
Best Local Similarity: 54.55% Mismatches: 5
Query Match: 37.76% Indels: 3
DB: 4 Gaps: 1

US-10-014-101B-32 (1-28) x US-09-949-016-12545 (1-163662)

QY 7 LeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMetSer-----AlaMet 23
Db 121684 TTGCAATACAAAAGGAGAGGACAAATGGGACAATTGATGTACATACGGCTGCTATG 121625
QY 24 IlePro 25
Db 121624 GTCCCT 121619

RESULT 7

US-09-949-016-13546/c
Sequence 13546, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

[illegible]

/	LOCATION: (81)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (90)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (93)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (96)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (99)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (105)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (108)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (111)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (114)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (117)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (120)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (123)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (126)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (129)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (135)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (141)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (144)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (147)	
/	OTHER INFORMATION: a,g,c o r t	
/	FEATURE:	
/	NAME/KEY: variation	
/	LOCATION: (153)	

QY 24 IleProGluIleAsp 28
Db 1336 ACGCCGCTGTGAGGAC 1350

RESULT 2
US-09-663-326-3
; Sequence 3, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-663-326-3

Alignment Scores:
Pred. No.: 0.578 Length: 1605
Score: 63.00 Matches: 11
Percent Similarity: 64.00% Conservative: 5
Best Local Similarity: 44.00% Mismatches: 9
Query Match: 42.86% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-663-326-3 (1-1605)

QY 4 GlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
Db 1276 GGCCCGCTCATGCTACCCCTCAACAAATCCATGTGGGACGACGGCATGTCTGGCGGCG 1335

QY 24 IleProGluIleAsp 28
Db 1336 ACGCCGCTGTGAGGAC 1350

RESULT 3
US-09-124-541-10
; Sequence 10, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: variation
; LOCATION: (6)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (9)
; OTHER INFORMATION: a,g,c or t
; FEATURE:

; NAME/KEY: variation
; LOCATION: (12)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (21)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (24)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (27)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (30)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (33)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (36)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (42)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (54)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (57)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (60)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (63)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (66)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (69)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (72)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (75)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (78)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 09:41:47 ; Search time 469 Seconds
(without alignments)
97.688 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRNKWNRMSAMPEID 28

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	63	42.9	1605	US-09-663-326-3	Sequence 3, Appli
3	58	39.5	1602	US-09-124-541-10	Sequence 10, Appl
4	58	39.5	1602	US-09-663-326-10	Sequence 10, Appl
5	55.5	37.8	601	US-09-949-016-62602	Sequence 62602, A
6	55.5	37.8	163662	US-09-949-016-12545	Sequence 12545, A
7	55.5	37.8	163664	US-09-949-016-13546	Sequence 13546, A
8	55	37.4	677	US-08-248-466B-4	Sequence 4, Appli
9	55	37.4	2763	US-08-248-466B-2	Sequence 2, Appli
10	55	37.4	32616	US-09-949-016-13407	Sequence 13407, A
11	54	36.7	1031	US-09-023-655-543	Sequence 543, App
12	54	36.7	28555	US-09-949-016-13046	Sequence 13046, A

C 13	53.5	36.4	3306	1	US-08-261-206A-71	Sequence 71, Appl
C 14	52	35.4	5198	1	US-08-123-761A-1	Sequence 1, Appli
C 15	52	35.4	84870	4	US-09-949-016-17547	Sequence 17547, A
C 16	51	34.7	1893	4	US-09-657-252-3	Sequence 3, Appli
C 17	51	34.7	53394	4	US-09-949-016-15817	Sequence 15817, A
C 18	51	34.7	53394	4	US-09-949-016-15818	Sequence 15818, A
C 19	51	34.7	53394	4	US-09-949-016-15819	Sequence 15819, A
C 20	51	34.7	53394	4	US-09-949-016-15820	Sequence 15820, A
C 21	51	34.7	62909	4	US-09-596-002-32	Sequence 32, Appl
C 22	50	34.0	510	4	US-09-902-540-6994	Sequence 6994, Ap
23	50	34.0	547	4	US-09-663-600A-137	Sequence 137, App
24	50	34.0	648	4	US-09-663-600A-43	Sequence 43, Appl
25	50	34.0	1008	4	US-09-248-796A-738	Sequence 738, App
26	50	34.0	2085	4	US-09-149-718-1	Sequence 1, Appli
27	50	34.0	2388	4	US-09-902-540-611	Sequence 611, App
28	50	34.0	390416	4	US-09-949-016-16923	Sequence 16923, A
29	49.5	33.7	6439	4	US-09-902-540-813	Sequence 813, App
C 30	49.5	33.7	27579	4	US-09-949-016-13465	Sequence 13465, A
31	49.5	33.7	141115	4	US-09-949-016-17490	Sequence 17490, A
32	49	33.3	120	1	US-08-458-516-21	Sequence 21, Appl
33	49	33.3	350	4	US-09-270-767-1938	Sequence 1938, Ap
34	49	33.3	350	4	US-09-270-767-17220	Sequence 17220, A
C 35	49	33.3	858	4	US-09-543-681A-925	Sequence 925, App
36	49	33.3	863	3	US-08-728-603-18	Sequence 18, Appl
C 37	49	33.3	948	4	US-09-489-039A-2926	Sequence 2926, Ap
38	49	33.3	1413	4	US-09-543-681A-3221	Sequence 3221, Ap
C 39	49	33.3	2601	3	US-09-221-017B-1014	Sequence 1014, Ap
C 40	49	33.3	32207	2	US-08-770-379-20	Sequence 20, Appl
C 41	49	33.3	32207	3	US-08-757-669A-20	Sequence 20, Appl
C 42	49	33.3	32207	3	US-09-230-371A-20	Sequence 20, Appl
C 43	49	33.3	192506	4	US-09-949-016-15830	Sequence 15830, A
C 44	48.5	33.0	137949	4	US-09-949-016-12196	Sequence 12196, A
C 45	48.5	33.0	137956	4	US-09-949-016-17260	Sequence 17260, A

ALIGNMENTS

RESULT 1
US-09-124-541-3
; Sequence 3, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-124-541-3

Alignment Scores:
Pred. No.: 0.578 Length: 1605
Score: 63.00 Matches: 11
Percent Similarity: 64.00% Conservative: 5
Best Local Similarity: 44.00% Mismatches: 9
Query Match: 42.86% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-124-541-3 (1-1605)

Qy 4 GlyLeuAlaLeuLeuTyPrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
Db 1276 GGCCCGTCATCGTCTACCCCTCAACAATCCATCGTGGACGACGGCG 1335

XX (PHAA) PHARMACIA CORP.
PA
XX
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX
DR WPI; 2003-897983/82.
DR GENBANK; AY091158.
XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Disclosure; SEQ ID NO 21; 33pp; English.
XX
CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 1873 BP; 495 A; 385 C; 482 G; 511 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.189 Length: 1873
Score: 69.00 Matches: 12
Percent Similarity: 75.00% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 46.94% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-32 (1-28) x ADH61280 (1-1873)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1340 AATGTTCCAATGCTTGTGTACCACTCTTGGAGACGAGGATGATCGGACGTCCTG 1399

Qy 23 MetIleProGlu 26
Db 1400 GTTATACCGAA 1411

Search completed: February 18, 2005, 10:16:45
Job time : 264 secs

XX 28-AUG-2003.
PD 20-DEC-2002; 2002US-00326184.
XX PF
XX 20-DEC-2001; 2001US-0343129P.
XX PR
XX (PHAA) PHARMACIA CORP.
XX PA
XX Huang S, Crossland LD, Cheikh N, Morris RO;
XX PI
XX WPI; 2003-897983/82.
DR GENBANK; AF540382.
XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
XX Disclosure; SEQ ID NO 22; 33pp; English.
PS The invention relates to a method for producing a plant characterised by
XX reversible male-sterility which involves transforming a plant cell with a
XX nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is barley cytokinin oxidase (CKX1) DNA. This sequence is used to
CC illustrate the method of the invention.
XX
SQ Sequence 1857 BP; 521 A; 454 C; 437 G; 445 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0173 Length: 1857
Score: 75.00 Matches: 12
Percent Similarity: 75.00% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 51.02% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-32 (1-28) x ADH61281 (1-1857)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1298 AATGGTCCCATATTGCTCTACCCAGTGAAGAAGTCCAGATGGGACAAACCGACGTG 1357
QY 23 MetIleProGlu 26
Db 1358 GTCATACCAAGAT 1369

RESULT 39
ADH61270
ID ADH61270 standard; DNA; 1575 BP.
XX
AC ADH61270;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #4.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2003163847-A1.
XX
XX 28-AUG-2003.

PF 20-DEC-2002; 2002US-00326184.
XX 20-DEC-2001; 2001US-0343129P.
XX (PHAA) PHARMACIA CORP.
XX Huang S, Crossland LD, Cheikh N, Morris RO;
XX WPI; 2003-897983/82.
DR GENBANK; AF303981.
XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Claim 44; SEQ ID NO 11; 33pp; English.
XX
CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 1575 BP; 390 A; 328 C; 451 G; 406 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.151 Length: 1575
Score: 69.00 Matches: 12
Percent Similarity: 75.00% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 46.94% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-32 (1-28) x ADH61270 (1-1575)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1225 AATGGTCCCAATGCTTGTGTACCCACTCTTGCAGACAGGTGGGATGATCGACGTCG 1284
QY 23 MetIleProGlu 26
Db 1285 GTTATACCGAA 1296

RESULT 40
ADH61280
ID ADH61280 standard; DNA; 1873 BP.
XX
AC ADH61280;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #7.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.
XX
PR 20-DEC-2001; 2001US-0343129P.

KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX Arabidopsis thaliana.
PN WO2003050287-A2.
XX WO2003050287-A2.
PD 19-JUN-2003.
XX 19-JUN-2003.
PF 10-DEC-2002; 2002WO-EP013990.
XX 10-DEC-2002; 2002WO-EP013990.
PR 10-DEC-2001; 2001US-00014101.
XX 10-DEC-2001; 2001US-00014101.
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX Schmullling T, Werner T;
PI Schmullling T, Werner T;
XX Schmullling T, Werner T;
DR WPI; 2003-541577/51.
XX WPI; 2003-541577/51.
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 174-175; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1620 BP; 419 A; 380 C; 411 G; 410 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00653 Length: 1620
Score: 77.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 52.38% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x ACC85301 (1-1620)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1222 AGTGGCCCTATTCTTATCTACCCCATGAACAAGACAAATGGGACGAGGAGCTCAGCC 1281
Qy 23 MetIleProGlu 26
Db 1282 GTGACGCCGGAT 1293

RESULT 37
ADH61271
ID ADH61271 standard; DNA; 1623 BP.
XX
AC ADH61271;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #5.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX

OS Arabidopsis thaliana.
XX Arabidopsis thaliana.
PN US2003163847-A1.
XX US2003163847-A1.
PD 28-AUG-2003.
XX 28-AUG-2003.
PF 20-DEC-2002; 2002US-00326184.
XX 20-DEC-2002; 2002US-00326184.
PR 20-DEC-2001; 2001US-0343129P.
XX 20-DEC-2001; 2001US-0343129P.
PA (PHAA) PHARMACIA CORP.
XX (PHAA) PHARMACIA CORP.
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX Huang S, Crossland LD, Cheikh N, Morris RO;
DR WPI; 2003-897983/82.
XX WPI; 2003-897983/82.
DR GENBANK; AF303982.
XX GENBANK; AF303982.
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Claim 45; SEQ ID NO 12; 33pp; English.
XX
CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 1623 BP; 421 A; 382 C; 412 G; 408 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00655 Length: 1623
Score: 77.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 52.38% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-32 (1-28) x ADH61271 (1-1623)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1225 AGTGGCCCTATTCTTATCTACCCCATGAACAAGACAAATGGGACGAGGAGCTCAGCC 1284
Qy 23 MetIleProGlu 26
Db 1285 GTGACGCCGGAT 1296

RESULT 38
ADH61281
ID ADH61281 standard; DNA; 1857 BP.
XX
AC ADH61281;
XX
DT 25-MAR-2004 (first entry)
XX
DE Barley cytokinin oxidase (CKX1) DNA #1.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; barley; ds; gene.
XX
OS Hordeum vulgare.
XX
PN US2003163847-A1.

XX PD 19-JUN-2003.
XX PF 10-DEC-2002; 2002WO-EP013990.
XX PR 10-DEC-2001; 2001US-00014101.
XX PA (SCHM/) SCHMULLING T.
XX PA (WERN/) WERNER T.
XX PI Schmullling T, Werner T;
XX XX WPI; 2003-541577/51.
XX DR Stimulating root growth, enhancing lateral or adventitious root formation
XX PT or altering root geotropism comprises increasing plant cytokinin oxidase
XX PT levels or other protein or nucleic acid that reduces active cytokinins in
XX PT a plant.
XX PS Claim 3; Page 170-171; 177pp; English.
XX CC The present invention relates to a method for stimulating root growth or
XX CC enhancing the formation of lateral or adventitious roots or altering root
XX CC geotropism, which comprises increasing in a plant or plant part the level
XX CC of a plant cytokinin oxidase or other protein that reduces the level of
XX CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
XX CC coding sequences from Arabidopsis thaliana are also provided. The method
XX CC is useful in modifying plant morphological, biochemical and physiological
XX CC properties, such as in modifying the initiation, stimulation or
XX CC enhancement of root growth, adventitious root formation, lateral root
XX CC formation, root geotropism, shoot growth, apical dominance, branching,
XX CC timing of senescence, timing of flowering, flower formation, seed
XX CC development and/or seed yield. The present sequence is a coding sequence
XX CC shown in the invention
XX SQ Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.00648 Length: 1611
Score: 77.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 52.38% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-32 (1-28) x ACC85297 (1-1611)
QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1213 AGTGGCCCTATTCTTATCTACCCCATGAACAAAGACAAATGGGACGAGAGCTCAGCC 1272
QY 23 MetIleProGlu 26
Db 1273 GTGACGCCGGAT 1284
RESULT 35
ID ABK28632 standard; cDNA; 1620 BP.
XX AC ABK28632;
XX XX 09-APR-2002 (first entry)
XX DE cDNA encoding A. thaliana cytokinin oxidase AtCKX5 (long version).
XX KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
XX KW root growth; lateral root; adventitious root; root geotropism; herbicide;
XX KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX OS Arabidopsis thaliana.
XX XX WO200196580-A2.
XX PN

PD 20-DEC-2001.
XX 18-JUN-2001; 2001WO-EP006833.
XX PF 16-JUN-2000; 2000EP-00870132.
XX PR 27-DEC-2000; 2000US-0258415P.
XX PR 16-MAR-2001; 2001EP-00870053.
XX (SCHM/) SCHMULLING T.
XX PA (WERN/) WERNER T.
XX PI Schmullling T, Werner T;
XX XX WPI; 2002-130736/17.
XX DR P-PSDB; AAU81974.
XX DR Polynucleotide encoding novel plant protein having cytokinin oxidase
XX PT activity and the protein useful for stimulating root growth, enhancing
XX PT the formation of lateral or adventitious roots, altering root geotropism.
XX PS Claim 3; Page 151; 154pp; English.
XX CC The invention relates to an isolated polynucleotide (I) encoding a novel
XX CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
XX CC production of transgenic plants, plant cells or tissues; for production
XX CC of altered plants, plant cell or tissues; and for effecting the
XX CC expression of (II) where (I) is operably linked to one or more control
XX CC sequences. The methods further comprises regenerating a plant from the
XX CC plant cell. (I) and (II) are useful for stimulating root growth;
XX CC enhancing the formation of lateral or adventitious roots; altering root
XX CC geotropism, leading to an increase in yield; and for screening growth
XX CC promoting chemical of herbicides. (I) is useful for increasing the size
XX CC of the root meristem; increasing root size; increasing the size of the
XX CC shoot meristem; delaying leaf senescence and altering leaf senescence;
XX CC increasing leaf thickness; reducing or increasing the vessel size;
XX CC inducing parthenocarp; improving standability of the seedlings;
XX CC increasing branching and for improving lodging resistance. Antibody (III)
XX CC to (II) is useful for identifying and obtaining proteins interacting with
XX CC (II) comprising a screening assay, preferably a two-hybrid screening
XX CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
XX CC coding sequences and PCR primers of the invention
XX SQ Sequence 1620 BP; 419 A; 380 C; 411 G; 410 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.00653 Length: 1620
Score: 77.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 52.38% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-32 (1-28) x ABK28632 (1-1620)
QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1222 AGTGGCCCTATTCTTATCTACCCCATGAACAAAGACAAATGGGACGAGAGCTCAGCC 1281
QY 23 MetIleProGlu 26
Db 1282 GTGACGCCGGAT 1293
RESULT 36
ID ACC85301 standard; cDNA; 1620 BP.
XX AC ACC85301;
XX XX 18-SEP-2003 (first entry)
XX DE Arabidopsis cytokinin oxidase-like protein 5 cDNA #2.
XX KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;

XX The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The
CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequences.html?DocID=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.
XX
SQ Sequence 788 BP; 218 A; 168 C; 185 G; 217 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00116 Length: 788
Score: 79.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 53.74% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-32 (1-28) x ADR61296 (1-788)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 412 AGTGGCCCAATTCATCTATCCATGAACAAGACAAATGGGACCATAGGAGCTCCGTC 471

Qy 23 MetIleProGlu 26

Db 472 GTGACACCGGAT 483

RESULT 33
ABK28628
ID ABK28628 standard; cDNA; 1611 BP.
XX
AC ABK28628;

DT 09-APR-2002 (first entry)

XX cDNA encoding A. thaliana cytokinin oxidase AtCKX5.
DE
XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX Arabidopsis thaliana.

OS WO200196580-A2.

XX 20-DEC-2001.

PN 18-JUN-2001; 2001WO-EP006833.

PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

PI WPI; 2002-130736/17.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.

PS Claim 3; Page 148-149; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX

SQ Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00648 Length: 1611
Score: 77.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 52.38% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x ABK28628 (1-1611)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1213 AGTGGCCCTATTCTTATCTACCCATGAACAAGACAAATGGGACGAGGAGCTCAGCC 1272

Qy 23 MetIleProGlu 26

Db 1273 GTGACGCCGGAT 1284

RESULT 34
ACC85297

ID ACC85297 standard; cDNA; 1611 BP.

XX ACC85297;

XX 18-SEP-2003 (first entry)

DE Arabidopsis cytokinin oxidase-like protein 5 cDNA #1.

XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

XX Arabidopsis thaliana.

XX WO2003050287-A2.

OS Arabidopsis thaliana.
XX WO2003050287-A2.
PN
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2003-541577/51.
DR P-PSDB; ABR63571.
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 2; Page 153-154; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 2782 BP; 826 A; 538 C; 507 G; 911 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00121 Length: 2782
Score: 83.00 Matches: 19
Percent Similarity: 37.93% Conservative: 3
Best Local Similarity: 32.76% Mismatches: 6
Query Match: 56.46% Indels: 30
DB: 9 Gaps: 1

US-10-014-101B-32 (1-28) x ACC85278 (1-2782)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2357 TCAACTTCTGGTGTACTCTCTCTATCCCAAAACCGAAACAAGTAAATATTTACTTTT 2416
QY 15 ----- 15
Db 2417 TGATTTGTTTTATTGTGAAAGTATATCCCAATAATGTATGTTAAATTTGTTAACAAGAATT 2476
QY 16 -----TTPAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2477 TATTTTATTAATAGATGGAACAACCGCATGTCAACGATGACACCGGACGAAGAT 2530
RESULT 28
ABK28629
ID ABK28629 standard; cDNA; 1515 BP.
XX
AC ABK28629;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX6.
XX

KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2002-130736/17.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Example 1; Page 149; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1515 BP; 456 A; 327 C; 378 G; 354 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00182 Length: 1515
Score: 80.00 Matches: 12
Percent Similarity: 80.77% Conservative: 9
Best Local Similarity: 46.15% Mismatches: 5
Query Match: 54.42% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x ABK28629 (1-1515)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTTPAspAsnArgMet 20
Db 1150 ACAAGCAACGGCCCGTCATCGTCTACCCAGTGAACAATCAAAGTGGACAATCAACA 1209
QY 21 SerAlaMetIleProGlu 26
Db 1210 TCAGCAGTAACACCGGAG 1227

RESULT 29
ACC85298
ID ACC85298 standard; cDNA; 1515 BP.
XX

PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 4438; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1566 BP; 422 A; 391 C; 371 G; 382 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000576 Length: 1566
Score: 83.00 Matches: 14
Percent Similarity: 76.92% Conservative: 6
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 56.46% Indels: 0
DB: 8

US-10-014-101B-32 (1-28) x ADA71115 (1-1566)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1201 AGTAACAATGGTCCCATATTACTCTATCCAGTGAACAAATCCAGATGGGACACAGAACA 1260

Qy 21 SerAlaMetIleProGlu 26
Db 1261 TCAGTAGTCATACCAGAT 1278

RESULT 26
ABK28609
ID ABK28609 standard; DNA; 2782 BP.
XX
AC ABK28609;
XX
DT 09-APR-2002 (first entry)
XX
DE DNA encoding A. thaliana cytokinin oxidase AtCKX4.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmulling T, Werner T;
DR WPI; 2002-130736/17.
DR P-PSDB; AAU81970.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 134-135; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 2782 BP; 826 A; 538 C; 507 G; 911 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00121 Length: 2782
Score: 83.00 Matches: 19
Percent Similarity: 37.93% Conservative: 3
Best Local Similarity: 32.76% Mismatches: 6
Query Match: 56.46% Indels: 30
DB: 6

US-10-014-101B-32 (1-28) x ABK28609 (1-2782)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2357 TCAACTTCTGGTGTACTCTCTCTATCCACAAACCGAAACAAAGTAATATTACTTTT 2416
Qy 15 ----- 15
Db 2417 TGATTTGTTTATTGAAAGTATATCCCAATAATGTAATGTTAAATTTGTTAACAAGATT 2476
Qy 16 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2477 TATTTTATTATAGATGGAACAACCGCATGTCAACGATGACACCGGACGAAGAT 2530

RESULT 27
ACC85278
ID ACC85278 standard; DNA; 2782 BP.
XX
AC ACC85278;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 4 gene.
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.
XX

OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 64..1761
FT /*tag= a
FT /product= "Rice grain number/cytokinin oxidase (CKX)-
FT related protein - SEQ ID 3"
XX
XX
PN WO2004044200-A1.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-JP014434.
XX PF
XX 13-NOV-2002; 2002US-0425919P.
XX PR
XX (HONDA) HONDA MOTOR CO LTD.
XX PA
XX Ashikari M, Matsuoka M, Lin S, Yamamoto T, Nishimura A,
PI Takashi T;
XX
DR WPI; 2004-420329/39.
DR P-PSDB; ADP03323.
XX
XX Cytokinin oxidase DNA which encodes plant derived protein (CKX) whose
PT functional deletion causes increase in number of grain arrivals in plant,
PT useful for improving plant varieties.
XX
XX Claim 1; SEQ ID NO 2; 89pp; Japanese.
XX
XX The invention relates to a novel cytokinin oxidase (CKX) DNA which
CC encodes the plant-derived protein whose functional deletion causes an
CC increase in the grain number of the plant, including glumous flower,
CC fruit and seed. The molecules of the invention may be useful for
CC producing a transformed plant. Thus, the molecules may be useful for
CC increasing the grain number of a plant and for improving plant varieties.
CC The current sequence is that of the rice grain number/cytokinin oxidase
CC (CKX)-related cDNA (SEQ ID 2) of the invention.
XX
SQ Sequence 2302 BP; 428 A; 707 C; 718 G; 449 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000193 Length: 2302
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservative: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-32 (1-28) x ADP03322 (1-2302)

QY 2 AlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
Db 1402 GCCATGGGCCCGCTCTCATCTACCCCATGAACCGCAACAAGTGGGACAGTACATGTCG 1461

QY 22 AlaMetIleProGluIleAsp 28
Db 1462 GCAGTGATCACCGACGACGAC 1482

RESULT 24
ADA69574
ID ADA69574 standard; DNA; 1587 BP.
XX
AC ADA69574;
XX
XX 20-NOV-2003 (first entry)
XX
XX Rice gene, SEQ ID 2897.
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.

XX WO2003000898-A1.
PN
XX 03-JAN-2003.
PD
XX 22-JUN-2001; 2001WO-IB001105.
PF
XX 22-JUN-2001; 2001WO-IB001105.
PR
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
DR
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 6; SEQ ID NO 2897; 899pp; English.
PS
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1587 BP; 307 A; 462 C; 458 G; 356 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 0.000265 Length: 1587
Score: 85.00 Matches: 14
Percent Similarity: 80.00% Conservative: 6
Best Local Similarity: 56.00% Mismatches: 5
Query Match: 57.82% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x ADA69574 (1-1587)

QY 4 GlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
Db 1255 GGCCTCATCTCATGTACCCCATGAATAAGGACATGTGGGATGACAGGATGACGGCGATG 1314

QY 24 IleProGluIleAsp 28
Db 1315 AGCCCGACGAGGAC 1329

RESULT 25
ADA71115
ID ADA71115 standard; DNA; 1566 BP.
XX
AC ADA71115;
XX
XX 20-NOV-2003 (first entry)
XX
XX Rice gene, SEQ ID 4438.
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
XX Oryza sativa.
XX
XX WO2003000898-A1.
XX
PD 03-JAN-2003.
XX

XX Rice gene, SEQ ID 3500.
DE
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 3500; 899pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1677 BP; 219 A; 608 C; 582 G; 267 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 0.000128 Length: 1677
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservative: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x ADA70177 (1-1677)

QY 2 AlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
Db 1318 GCCATGGGCCCCGTCCTCATCTACCCCATGAACCGCAACAAAGTGGGACAGTAACATGTCG 1377
QY 22 AlaMetIleProGluIleAsp 28
Db 1378 GCAGTGATCACCGACGACGAC 1398

RESULT 22
ADP03325
ID ADP03325 standard; cDNA; 2282 BP.
XX
AC ADP03325;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rice grain number/cytokinin oxidase (CKX)-related cDNA - SEQ ID 5.
XX
KW cytokinin oxidase; CKX; grain number; plant; glumous flower; fruit; seed;
KW transgenic; rice; ss; gene.

XX Oryza sativa.
OS
XX
FH Key Location/Qualifiers
FT CDS 48..1739
FT /*tag= a
FT /product= "Rice grain number/cytokinin oxidase (CKX) -
XX related protein - SEQ ID 6"
PN WO2004044200-A1.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-JP014434.
XX
PR 13-NOV-2002; 2002US-0425919P.
XX
PA (HOND) HONDA MOTOR CO LTD.
XX
PI Ashikari M, Matsuoka M, Lin S, Yamamoto T, Nishimura A;
PI Takashi T;
XX
DR WPI; 2004-420329/39.
DR P-PSDB; ADP03326.
XX
PT Cytokinin oxidase DNA which encodes plant derived protein (CKX) whose
PT functional deletion causes increase in number of grain arrivals in plant,
PT useful for improving plant varieties.
XX
PS Disclosure; SEQ ID NO 5; 89pp; Japanese.
XX
CC The invention relates to a novel cytokinin oxidase (CKX) DNA which
CC encodes the plant-derived protein whose functional deletion causes an
CC increase in the grain number of the plant, including glumous flower,
CC fruit and seed. The molecules of the invention may be useful for
CC producing a transformed plant. Thus, the molecules may be useful for
CC increasing the grain number of a plant and for improving plant varieties.
CC The current sequence is that of the rice grain number/cytokinin oxidase
CC (CKX)-related cDNA (SEQ ID 5) of the invention.
XX
SQ Sequence 2282 BP; 423 A; 701 C; 715 G; 443 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000191 Length: 2282
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservative: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-32 (1-28) x ADP03325 (1-2282)

QY 2 AlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
Db 1380 GCCATGGGCCCCGTCCTCATCTACCCCATGAACCGCAACAAAGTGGGACAGTAACATGTCG 1439
QY 22 AlaMetIleProGluIleAsp 28
Db 1440 GCAGTGATCACCGACGACGAC 1460

RESULT 23
ADP03322
ID ADP03322 standard; cDNA; 2302 BP.
XX
AC ADP03322;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rice grain number/cytokinin oxidase (CKX)-related cDNA - SEQ ID 2.
XX
KW cytokinin oxidase; CKX; grain number; plant; glumous flower; fruit; seed;
KW transgenic; rice; ss; gene.

XX 20-DEC-2001.
XX PD
XX PF
XX PR 18-JUN-2001; 2001WO-EP006833.
XX PR 16-JUN-2000; 2000EP-00870132.
XX PR 27-DEC-2000; 2000US-0258415P.
XX PR 16-MAR-2001; 2001EP-00870053.
XX PA (SCHM//) SCHMULLING T.
XX PA (WERN//) WERNER T.
XX PI
XX PI Schmullling T, Werner T;
XX DR WPI; 2002-130736/17.
XX DR P-PSDB; AAU81968.
XX PT Polynucleotide encoding novel plant protein having cytokinin oxidase
XX PT activity and the protein useful for stimulating root growth, enhancing
XX PT the formation of lateral or adventitious roots, altering root geotropism.
XX PS Claim 3; Page 128-129; 154pp; English.
XX CC The invention relates to an isolated polynucleotide (I) encoding a novel
XX CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
XX CC production of transgenic plants, plant cells or tissues; for production
XX CC of altered plants, plant cell or tissues; and for effecting the
XX CC expression of (II) where (I) is operably linked to one or more control
XX CC sequences. The methods further comprises regenerating a plant from the
XX CC plant cell. (I) and (II) are useful for stimulating root growth;
XX CC enhancing the formation of lateral or adventitious roots; altering root
XX CC geotropism; leading to an increase in yield; and for screening growth
XX CC promoting chemical of herbicides. (I) is useful for increasing the size
XX CC of the root meristem; increasing root size; increasing the size of the
XX CC shoot meristem; delaying leaf senescence and altering leaf senescence;
XX CC increasing leaf thickness; reducing or increasing the vessel size;
XX CC inducing parthenocarp; improving standability of the seedlings;
XX CC increasing branching and for improving lodging resistance. Antibody (III)
XX CC to (II) is useful for identifying and obtaining proteins interacting with
XX CC (II) comprising a screening assay, preferably a two-hybrid screening
XX CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
XX CC coding sequences and PCR primers of the invention
XX SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.22e-06 Length: 2991
Score: 96.50 Matches: 27
Percent Similarity: 48.21% Conservative: 0
Best Local Similarity: 48.21% Mismatches: 1
Query Match: 65.65% Indels: 29
DB: 6 Gaps: 1

US-10-014-101B-32 (1-28) x ABK28607 (1-2991)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2573 TCAGCTTCGGGACTCGCTCTTCTATCCAAACCAACCGGAATAA-GTACATACTTCTCTT 2631

QY 15 ----- 15
Db 2632 CATTCAATTTATCTTCAAGAACCAAGTAAATAATTTCTATGAAGTATTGCTGTT 2691

QY 16 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2692 ATTGTTAGATGGGACAATCGTATGTCGGCGATGATACCAGAGATCGAT 2739

RESULT 16
ACC85276
ID ACC85276 standard; DNA; 2991 BP.
XX AC ACC85276;
XX

DT 18-SEP-2003 (first entry)
XX Arabidopsis cytokinin oxidase-like protein 2 gene.
DE Maize; root growth; root geotropism; cytokinin oxidase; seed size;
XX KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.
XX OS Arabidopsis thaliana.
XX PN WO2003050287-A2.
XX PD 19-JUN-2003.
XX PF 10-DEC-2002; 2002WO-EP013990.
XX PR 10-DEC-2001; 2001US-00014101.
XX PA (SCHM//) SCHMULLING T.
XX PA (WERN//) WERNER T.
XX PI Schmullling T, Werner T;
XX DR WPI; 2003-541577/51.
XX DR P-PSDB; ABR63569.
XX PT Stimulating root growth, enhancing lateral or adventitious root formation
XX PT or altering root geotropism comprises increasing plant cytokinin oxidase
XX PT levels or other protein or nucleic acid that reduces active cytokinins in
XX PT a plant.
XX PS Claim 3; Page 145-146; 177pp; English.
XX CC The present invention relates to a method for stimulating root growth or
XX CC enhancing the formation of lateral or adventitious roots or altering root
XX CC geotropism, which comprises increasing in a plant or plant part the level
XX CC of a plant cytokinin oxidase or other protein that reduces the level of
XX CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
XX CC coding sequences from Arabidopsis thaliana are also provided. The method
XX CC is useful in modifying plant morphological, biochemical and physiological
XX CC properties, such as in modifying the initiation, stimulation or
XX CC enhancement of root growth, adventitious root formation, lateral root
XX CC formation, root geotropism, shoot growth, apical dominance, branching,
XX CC timing of senescence, timing of flowering, flower formation, seed
XX CC development and/or seed yield. The present sequence is a coding sequence
XX CC shown in the invention
XX SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.22e-06 Length: 2991
Score: 96.50 Matches: 27
Percent Similarity: 48.21% Conservative: 0
Best Local Similarity: 48.21% Mismatches: 1
Query Match: 65.65% Indels: 29
DB: 9 Gaps: 1

US-10-014-101B-32 (1-28) x ACC85276 (1-2991)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2573 TCAGCTTCGGGACTCGCTCTTCTATCCAAACCAACCGGAATAA-GTACATACTTCTCTT 2631

QY 15 ----- 15
Db 2632 CATTCAATTTATCTTCAAGAACCAAGTAAATAATTTCTATGAAGTATTGCTGTT 2691

QY 16 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2692 ATTGTTAGATGGGACAATCGTATGTCGGCGATGATACCAGAGATCGAT 2739

RESULT 17
ABK28626
ID ABK28626 standard; cDNA; 1572 BP.


```
XX ADA68648;
AC
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX Arabidopsis thaliana gene, SEQ ID 428.
DE
XX
XX Plant; bacterial infection; fungal infection; viral infection; ds.
KW
XX Arabidopsis thaliana.
OS
XX
XX WO2003000898-A1.
PN
XX
XX 03-JAN-2003.
PD
XX
XX 22-JUN-2001; 2001WO-IB001105.
PF
XX
XX 22-JUN-2001; 2001WO-IB001105.
PR
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
PI
XX WPI; 2003-175290/17.
DR
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 428; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.81e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x ADA68648 (1-1575)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTCTATCCCAACCGAACAATGGAACACCGCATG 1299
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 12
ACC85296
ID ACC85296 standard; cDNA; 1575 BP.
XX
AC ACC85296;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 4 cDNA.
```

```
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmulling T, Werner T;
XX WPI; 2003-541577/51.
DR
XX Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 2; Page 169-170; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.81e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x ACC85296 (1-1575)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTCTATCCCAACCGAACAATGGAACACCGCATG 1299
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 13
ADH61269
ID ADH61269 standard; DNA; 1575 BP.
XX
AC ADH61269;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #3.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
```

XX 21-JAN-2003 (first entry)
DT Arabidopsis thaliana stress regulated gene SEQ ID NO 2089.
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX Arabidopsis thaliana.
KW Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO200216655-A2.
XX 28-FEB-2002.
XX 24-AUG-2001; 2001WO-US026685.
PF 24-AUG-2000; 2000US-0227866P.
XX 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
PI WPI; 2002-304127/34.
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 2089; 577pp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.81e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x ABZ14284 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTCTATCCCAACCGAACAATGGAACAACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 10
ABK28627
ID ABK28627 standard; cDNA; 1575 BP.
XX
AC ABK28627;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX4.

XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO200196580-A2.
XX 20-DEC-2001.
XX 18-JUN-2001; 2001WO-EP006833.
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX Schmulling T, Werner T;
PI WPI; 2002-130736/17.
XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX Claim 2; Page 147-148; 154pp; English.
XX The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.81e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x ABK28627 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTCTATCCCAACCGAACAATGGAACAACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 11
ADA68648
ID ADA68648 standard; DNA; 1575 BP.

PR	13-SEP-1999;	99US-0153758P;
PR	15-SEP-1999;	99US-0154018P;
PR	16-SEP-1999;	99US-0154039P;
PR	20-SEP-1999;	99US-0154779P;
PR	22-SEP-1999;	99US-0155139P;
PR	23-SEP-1999;	99US-0155486P;
PR	24-SEP-1999;	99US-0155659P;
PR	28-SEP-1999;	99US-0156458P;
PR	29-SEP-1999;	99US-0156596P;
PR	04-OCT-1999;	99US-0157117P;
PR	05-OCT-1999;	99US-0157753P;
PR	06-OCT-1999;	99US-0157865P;
PR	07-OCT-1999;	99US-0158029P;
PR	08-OCT-1999;	99US-0158232P;
PR	12-OCT-1999;	99US-0158369P;
PR	13-OCT-1999;	99US-0159293P;
PR	13-OCT-1999;	99US-0159294P;
PR	13-OCT-1999;	99US-0159295P;
PR	14-OCT-1999;	99US-0159329P;
PR	14-OCT-1999;	99US-0159330P;
PR	14-OCT-1999;	99US-0159331P;
PR	14-OCT-1999;	99US-0159637P;
PR	14-OCT-1999;	99US-0159638P;
PR	18-OCT-1999;	99US-0159584P;
PR	21-OCT-1999;	99US-0160741P;
PR	21-OCT-1999;	99US-0160767P;
PR	21-OCT-1999;	99US-0160768P;
PR	21-OCT-1999;	99US-0160770P;
PR	21-OCT-1999;	99US-0160814P;
PR	21-OCT-1999;	99US-0160815P;
PR	22-OCT-1999;	99US-0160980P;
PR	22-OCT-1999;	99US-0160981P;
PR	22-OCT-1999;	99US-0160989P;
PR	25-OCT-1999;	99US-0161404P;
PR	25-OCT-1999;	99US-0161405P;
PR	25-OCT-1999;	99US-0161406P;
PR	26-OCT-1999;	99US-0161359P;
PR	26-OCT-1999;	99US-0161360P;
PR	26-OCT-1999;	99US-0161361P;
PR	28-OCT-1999;	99US-0161920P;
PR	28-OCT-1999;	99US-0161992P;
PR	28-OCT-1999;	99US-0161993P;
PR	29-OCT-1999;	99US-0162142P;

US-10-014-101B-32 (1-28) x AAC43214 (1-1548)

Qy	1	SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn-----	14
Db	1171	TCAGCTTCGGGACTCGCTCTTCTATCCAAACAACCGGAATAAGTACATACTTCTCTTC	1230
Qy	15	-----LysTyrAspAsnArgMetSerAlaMetIleProGlu	26
Db	1231	ATTCATATTTATCTTCAAGAACCAAAATGGGACAATCGTATGTCCGGCGATGATACCAGAG	1290
Qy	27	IleAsp	28
Db	1291	ATCGAT	1296

RESULT 8

AAC42983

ID AAC42983 standard; DNA; 1575 BP.

XX

AC AAC42983;

XX

DT 17-OCT-2000 (first entry)

XX	Arabidopsis thaliana DNA frag
DE	Hybridisation assay; genetic
XX	protein identification; signal
KW	promoter; termination sequenc
KW	
XX	Arabidopsis thaliana.
OS	
XX	EP1033405-A2.
PN	
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
XX	
PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130510P.
PR	23-APR-1999; 99US-0130891P.
PR	28-APR-1999; 99US-0131449P.
PR	30-APR-1999; 99US-0132048P.
PR	30-APR-1999; 99US-0132407P.
PR	04-MAY-1999; 99US-0132484P.
PR	05-MAY-1999; 99US-0132485P.
PR	06-MAY-1999; 99US-0132486P.
PR	06-MAY-1999; 99US-0132487P.
PR	07-MAY-1999; 99US-0132863P.
PR	11-MAY-1999; 99US-0134256P.
PR	14-MAY-1999; 99US-0134218P.
PR	14-MAY-1999; 99US-0134219P.
PR	14-MAY-1999; 99US-0134221P.
PR	14-MAY-1999; 99US-0134370P.
PR	18-MAY-1999; 99US-0134768P.
PR	19-MAY-1999; 99US-0134941P.
PR	20-MAY-1999; 99US-0135124P.
PR	21-MAY-1999; 99US-0135353P.
PR	24-MAY-1999; 99US-0135629P.
PR	25-MAY-1999; 99US-0136021P.
PR	27-MAY-1999; 99US-0136392P.
PR	28-MAY-1999; 99US-0136782P.
PR	01-JUN-1999; 99US-0137222P.
PR	03-JUN-1999; 99US-0137528P.
PR	04-JUN-1999; 99US-0137502P.
PR	07-JUN-1999; 99US-0137724P.
PR	08-JUN-1999; 99US-0138094P.
PR	10-JUN-1999; 99US-0138540P.
PR	10-JUN-1999; 99US-0138847P.
PR	14-JUN-1999; 99US-0139119P.
PR	16-JUN-1999; 99US-0139452P.
PR	16-JUN-1999; 99US-0139453P.
PR	17-JUN-1999; 99US-0139492P.
PR	18-JUN-1999; 99US-0139454P.
PR	18-JUN-1999; 99US-0139455P.
PR	18-JUN-1999; 99US-0139456P.
PR	18-JUN-1999; 99US-0139457P.
PR	18-JUN-1999; 99US-0139458P.
PR	18-JUN-1999; 99US-0139459P.
PR	18-JUN-1999; 99US-0139461P.
PR	18-JUN-1999; 99US-0139462P.
PR	18-JUN-1999; 99US-0139463P.
PR	18-JUN-1999; 99US-0139750P.
PR	18-JUN-1999; 99US-0139763P.

XX	Arabidopsis thaliana.		
OS	EP1033405-A2.		
XX	06-SEP-2000.		
PN	25-FEB-2000; 2000EP-00301439.		
XX	25-FEB-1999;	99US-0121825P.	99US-0140991P.
PD	05-MAR-1999;	99US-0123180P.	99US-0141287P.
PF	09-MAR-1999;	99US-0123548P.	99US-0141842P.
XX	23-MAR-1999;	99US-0125788P.	99US-0142154P.
XX	25-MAR-1999;	99US-0126264P.	99US-0142055P.
XX	29-MAR-1999;	99US-0126785P.	99US-0142390P.
XX	01-APR-1999;	99US-0127462P.	99US-0142803P.
XX	06-APR-1999;	99US-0128234P.	99US-0142920P.
XX	08-APR-1999;	99US-0128714P.	99US-0142977P.
XX	16-APR-1999;	99US-0129845P.	99US-0143542P.
XX	19-APR-1999;	99US-0130077P.	99US-0143624P.
XX	21-APR-1999;	99US-0130449P.	99US-0144005P.
XX	23-APR-1999;	99US-0130510P.	99US-0144085P.
XX	23-APR-1999;	99US-0130891P.	99US-0144086P.
XX	28-APR-1999;	99US-0131449P.	99US-0144325P.
XX	30-APR-1999;	99US-0132048P.	99US-0144331P.
XX	30-APR-1999;	99US-0132407P.	99US-0144332P.
XX	04-MAY-1999;	99US-0132484P.	99US-0144333P.
XX	05-MAY-1999;	99US-0132485P.	99US-0144334P.
XX	06-MAY-1999;	99US-0132486P.	99US-0144335P.
XX	07-MAY-1999;	99US-0132863P.	99US-0144352P.
XX	11-MAY-1999;	99US-0134256P.	99US-0144632P.
XX	14-MAY-1999;	99US-0134218P.	99US-0145218P.
XX	14-MAY-1999;	99US-0134219P.	99US-0145224P.
XX	14-MAY-1999;	99US-0134221P.	99US-0145276P.
XX	14-MAY-1999;	99US-0134370P.	99US-0145913P.
XX	18-MAY-1999;	99US-0134768P.	99US-0145918P.
XX	19-MAY-1999;	99US-0134941P.	99US-0145919P.
XX	20-MAY-1999;	99US-0135124P.	99US-0145951P.
XX	21-MAY-1999;	99US-0135353P.	99US-0146386P.
XX	24-MAY-1999;	99US-0135629P.	99US-0146388P.
XX	25-MAY-1999;	99US-0136021P.	99US-0146389P.
XX	27-MAY-1999;	99US-0136392P.	99US-0147038P.
XX	28-MAY-1999;	99US-0136782P.	99US-0147204P.
XX	01-JUN-1999;	99US-0137222P.	99US-0147302P.
XX	03-JUN-1999;	99US-0137528P.	99US-0147192P.
XX	04-JUN-1999;	99US-0137502P.	99US-0147260P.
XX	07-JUN-1999;	99US-0137724P.	99US-0147303P.
XX	08-JUN-1999;	99US-0138094P.	99US-0147416P.
XX	10-JUN-1999;	99US-0138540P.	99US-0147493P.
XX	10-JUN-1999;	99US-0138847P.	99US-0147935P.
XX	14-JUN-1999;	99US-0139119P.	99US-0148171P.
XX	16-JUN-1999;	99US-0139452P.	99US-0148319P.
XX	16-JUN-1999;	99US-0139453P.	99US-0148341P.
XX	17-JUN-1999;	99US-0139492P.	99US-0148565P.
XX	18-JUN-1999;	99US-0139454P.	99US-0148684P.
XX	18-JUN-1999;	99US-0139455P.	99US-0149368P.
XX	18-JUN-1999;	99US-0139456P.	99US-0149175P.
XX	18-JUN-1999;	99US-0139457P.	99US-0149426P.
XX	18-JUN-1999;	99US-0139458P.	99US-0149722P.
XX	18-JUN-1999;	99US-0139459P.	99US-0149723P.
XX	18-JUN-1999;	99US-0139460P.	99US-0149929P.
XX	18-JUN-1999;	99US-0139461P.	99US-0149902P.
XX	18-JUN-1999;	99US-0139462P.	99US-0149930P.
XX	18-JUN-1999;	99US-0139463P.	99US-0150566P.
XX	18-JUN-1999;	99US-0139750P.	99US-0150884P.
XX	21-JUN-1999;	99US-0139763P.	99US-0151065P.
XX	22-JUN-1999;	99US-0139817P.	99US-0151066P.
XX	23-JUN-1999;	99US-0139899P.	99US-0151080P.
XX	23-JUN-1999;	99US-0140353P.	99US-0151303P.
XX	24-JUN-1999;	99US-0140354P.	99US-0151438P.
XX	28-JUN-1999;	99US-0140823P.	99US-0151930P.
XX			99US-0152363P.
XX			99US-0153070P.

XX 20-DEC-2001; 2001US-0343129P.
XX (PHAA) PHARMACIA CORP.
PA Huang S, Crossland LD, Cheikh N, Morris RO;
PI WPI; 2003-897983/82.
XX GENBANK; AF303978.
DR Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX Claim 41; SEQ ID NO 8; 33pp; English.
XX The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 1506 BP; 431 A; 329 C; 323 G; 423 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.91e-15 Length: 1506
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-014-101B-32 (1-28) x ADH61267 (1-1506)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1171 TCAGCTTCGGGACTCGCTCTCTCTATCCAAACCGGATAAATGGGACAATCGTATG 1230
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1231 TCGGCGATGATACCGAGATCGAT 1254
RESULT 6
ADO06498
ID ADO06498 standard; DNA; 1506 BP.
XX
AC ADO06498;
XX
DT 29-JUL-2004 (first entry)
XX
DE A thaliana cytokinin oxidase AtCKX2 coding sequence.
XX
KW bioremediation; AtCKX2; cytokinin availability; contaminant;
KW metal deficiency; nutrition; ds; gene; cytokinin oxidase.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 1..1506
FT /*tag= a
FT /product= "AtCKX2"
XX
PN WO2004038027-A1.
XX
PD 06-MAY-2004.

XX 24-OCT-2003; 2003WO-EP012051.
PF
XX
PR 24-OCT-2002; 2002EP-00079481.
XX
PA (CROP-) CROPDESIGN NV.
XX
PI Van Camp W;
XX
DR WPI; 2004-375913/35.
DR P-PSDB; ADO06499.
XX
PT Method for bioremediation, useful for removing contaminants or metals, by
PT decreasing cytokinin availability in plants, and cultivating plant on
PT substrate comprising one or more contaminants.
XX
PS Claim 8; Page 55; 61pp; English.
XX The present invention relates to a method for bioremediation, which
CC involves decreasing cytokinin availability in a plant relative to a
CC corresponding wild type plant, and cultivating the plant on a substrate
CC comprising one or more contaminants, or cultivating a plant having
CC lowered availability of cytokinin relative to corresponding wild type
CC plants, on a substrate, which is to be treated. The method is useful for
CC bioremediation, for concentration of contaminants in a plant, where the
CC plant has a higher concentration of contaminants compared to a
CC corresponding wild type plant. The metal contaminants include aluminum,
CC americium, antimony, arsenic, barium, beryllium, bismuth, cadmium,
CC caesium, cerium, chromium, copper, gallium, germanium, gold, indium,
CC iridium, iron, lead, manganese, mercury, molybdenum, neptunium, osmium,
CC palladium, platinum, plutonium, radium, rhenium, rhodium, rubidium,
CC ruthenium, scandium, selenium, silver, strontium, technetium, tellurium,
CC thallium, tin, tungsten, uranium, vanadium or yttrium, preferably
CC cadmium. The plant obtained by the method is useful in bioremediation.
CC Transgenic plants with a lower availability of cytokinin are useful in
CC the manufacture of a medicament for treatment of disorders arising from
CC metal deficiencies, and as a medicament for improving animal or human
CC nutrition. The present sequence is a coding sequence shown in the
CC exemplification of the invention.
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.91e-15 Length: 1506
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-014-101B-32 (1-28) x ADO06498 (1-1506)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1171 TCAGCTTCGGGACTCGCTCTCTCTATCCAAACCGGATAAATGGGACAATCGTATG 1230
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1231 TCGGCGATGATACCGAGATCGAT 1254
RESULT 7
AAC43214
ID AAC43214 standard; DNA; 1548 BP.
XX
AC AAC43214;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX WPI; 2002-130736/17.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 146-147; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarpy; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.91e-15 Length: 1506
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x ABK28625 (1-1506)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1171 TCAGCTTCGGGACTCGCTCTTCTCTATCCAAACCGGAATAAATGGGACATCGTATG 1230

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1231 TCGGCGATGATACCGAGATCGAT 1254

RESULT 4
ACC85294
ID ACC85294 standard; cDNA; 1506 BP.
XX
AC ACC85294;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 2 cDNA.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.
PF
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX WPI; 2003-541577/51.
DR
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 167-168; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.91e-15 Length: 1506
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x ACC85294 (1-1506)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1171 TCAGCTTCGGGACTCGCTCTTCTCTATCCAAACCGGAATAAATGGGACATCGTATG 1230

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1231 TCGGCGATGATACCGAGATCGAT 1254

RESULT 5
ADH61267
ID ADH61267 standard; DNA; 1506 BP.
XX
AC ADH61267;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #1.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.

PI Schmulling T, Werner T;
XX WPI; 2002-130736/17.
DR P-PSDB; AAU81973.
XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX Claim 3; Page 149; 154pp; English.
PS The invention relates to an isolated polynucleotide (I) encoding a novel
XX plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 84 BP; 24 A; 21 C; 19 G; 20 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.17e-16 Length: 84
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x ABK28630 (1-84)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1 TCAGCTTCGGGACTCGCTCTCTCTATCCAAACCGGAATAAATGGGACATCGTATG 60
Qy 21 SerAlaMetIleProGluIleAsp 28
Db 61 TCGGCGATGATACACAGATCGAT 84

RESULT 2
ACC85299
ID ACC85299 standard; CDNA; 84 BP.
XX
AC. ACC85299;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 2 cDNA fragment #1.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.

XX (SCHM//) SCHMULLING T.
PA (WERN//) WERNER T.
XX Schmulling T, Werner T;
PI WPI; 2003-541577/51.
XX Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX Claim 3; Page 172; 177pp; English.
PS The present invention relates to a method for stimulating root growth or
XX enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 84 BP; 24 A; 21 C; 19 G; 20 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.17e-16 Length: 84
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x ACC85299 (1-84)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1 TCAGCTTCGGGACTCGCTCTCTCTATCCAAACCGGAATAAATGGGACATCGTATG 60
Qy 21 SerAlaMetIleProGluIleAsp 28
Db 61 TCGGCGATGATACACAGATCGAT 84

RESULT 3
ABK28625
ID ABK28625 standard; CDNA; 1506 BP.
XX
AC. ABK28625;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX2.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 07:01:12 ; Search time 256 Seconds
(without alignments)
647.472 Million cell updates/sec

Title: US-10-014-101B-32
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	84	6 ABK28630	Abk28630 A. thalia
2	147	100.0	84	9 ACC85299	Acc85299 Arabidops
3	147	100.0	1506	6 ABK28625	Abk28625 cDNA enco
4	147	100.0	1506	9 ACC85294	Acc85294 Arabidops
5	147	100.0	1506	10 ADH61267	Adh61267 Arabidops

6	147	100.0	1506	12	ADO06498	Ado06498 A thalian
7	130	88.4	1548	3	AAC43214	Aac43214 Arabidops
8	108	73.5	1575	3	AAC42983	Aac42983 Arabidops
9	108	73.5	1575	6	ABZ14284	Abz14284 Arabidops
10	108	73.5	1575	6	ABK28627	Abk28627 cDNA enco
11	108	73.5	1575	8	ADA68648	Ada68648 Arabidops
12	108	73.5	1575	9	ACC85296	Acc85296 Arabidops
13	108	73.5	1575	10	ADH61269	Adh61269 Arabidops
14	108	73.5	1655	10	ADH61279	Adh61279 Arabidops
15	96.5	65.6	2991	6	ABK28607	Abk28607 DNA enco
16	96.5	65.6	2991	9	ACC85276	Acc85276 Arabidops
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18	96	65.3	1572	9	ACC85295	Acc85295 Arabidops
19	96	65.3	1572	10	ADH61268	Adh61268 Arabidops
20	88	59.9	1590	8	ADA69773	Ada69773 Rice gene
21	87	59.2	1677	8	ADA70177	Ada70177 Rice gene
22	87	59.2	2282	12	ADP03325	Adp03325 Rice grai
23	87	59.2	2302	12	ADP03322	Adp03322 Rice grai
24	85	57.8	1587	8	ADA69574	Ada69574 Rice gene
25	83	56.5	1566	8	ADA71115	Ada71115 Rice gene
26	83	56.5	2782	6	ABK28609	Abk28609 DNA enco
27	83	56.5	2782	9	ACC85278	Acc85278 Arabidops
28	80	54.4	1515	6	ABK28629	Abk28629 cDNA enco
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31	79	53.7	484	13	ACN55634	Acn55634 Cotton an
32	79	53.7	788	13	ADR61296	Adr61296 Cotton cd
33	77	52.4	1611	6	ABK28628	Abk28628 cDNA enco
34	77	52.4	1611	9	ACC85297	Acc85297 Arabidops
35	77	52.4	1620	6	ABK28632	Abk28632 cDNA enco
36	77	52.4	1620	9	ACC85301	Acc85301 Arabidops
37	77	52.4	1623	10	ADH61271	Adh61271 Arabidops
38	75	51.0	1857	10	ADH61281	Adh61281 Barley cy
39	69	46.9	1575	10	ADH61270	Adh61270 Arabidops
40	69	46.9	1873	10	ADH61280	Adh61280 Arabidops
41	68	46.3	413	10	ADH61283	Adh61283 Wheat cyt
42	68	46.3	413	10	ADH61282	Adh61282 Barley cy
43	68	46.3	573	13	ACN53055	Acn53055 Cotton an
44	68	46.3	581	13	ACN59325	Acn59325 Cotton gy
45	63	42.9	1605	2	AAX02914	Aax02914 Z. mays C

ALIGNMENTS

RESULT 1
ABK28630
ID ABK28630 standard; cDNA; 84 BP.
XX
AC ABK28630;
XX
DT 09-APR-2002 (first entry)
XX
DE A. thaliana cytokinin oxidase AtCKX2, cDNA fragment.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
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PA (WERN/) WERNER T.
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STS

ORIGIN

Alignment Scores:

Pred. No.: 0.00233 Length: 342
Score: 77.00 Matches: 15
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 93.75% Mismatches: 0
Query Match: 52.38% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-32 (1-28) x BX255834 (1-342)

QY

1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrp 16
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Db

243 TCAGCTTCGGGACTCGCTCTCTCTATCCAAACCGGATAAGTAC 290
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RESULT 40

BX255816

LOCUS

BX255816 366 bp DNA linear STS 11-JUN-2003

DEFINITION

Arabidopsis thaliana transposon insertion STS SM_3.25117, sequence tagged site.

ACCESSION

BX255816

VERSION

BX255816.1 GI:28411106

KEYWORDS

STS; STS, sequence tagged site.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B., Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M. Unpublished

JOURNAL

2 (bases 1 to 366)

AUTHORS

Clarke,J.H.

TITLE

Direct Submission

JOURNAL

Submitted (17-FEB-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

COMMENT

AT denotes an activation tag dissociation transposon within a single line, Et an enhancer trap dissociation transposon, Gt a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3'end of the transposon, _5 denotes a sequence derived from the 5'end of the transposon, BESRC GARNET, ATIS project
On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N111666.

FEATURES

source

location/Qualifiers

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/organism="Arabidopsis thaliana"
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/note="Derived from superpool 8.28 NASC code N40371"
1. .366
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STS

ORIGIN

Alignment Scores:

Pred. No.: 0.00252 Length: 366
Score: 77.00 Matches: 15
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 93.75% Mismatches: 0

Query Match:

52.38% Indels: 0

DB:

11 Gaps: 0

US-10-014-101B-32 (1-28) x BX255816 (1-366)

QY

1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrp 16
|||||

Db

243 TCAGCTTCGGGACTCGCTCTCTCTATCCAAACCGGATAAGTAC 290
|||||

Search completed: February 18, 2005, 12:07:21

Job time : 6634 secs

JOURNAL Submitted (06-APR-2001) Yang S., Department of Biological Sciences,
National University of Singapore, 119260, SINGAPORE
COMMENT On Apr 12, 2001 this sequence version replaced gi:11558276.
FEATURES Location/Qualifiers
source 1..1740
/organism="Dendrobium cv. 'Sonia'"
/mol_type="mRNA"
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34..1644
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34..1644
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ORIGIN

Alignment Scores:
Pred. No.: 0.00766 Length: 1866
Score: 79.00 Matches: 12
Percent Similarity: 79.17% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 53.74% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x AY209184 (1-1866)

Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1292 AATGGTCCCATATTGCTCTACCCAGTGAACAAGTCCAGATGGGACCAACCATCAGTG 1351
Qy 23 MetIleProGlu 26
Db 1352 GTCTTACCAGAT 1363

RESULT 39
BX255834

LOCUS Arabidopsis thaliana transposon insertion STS SM_3.25119, sequence
DEFINITION tagged site.
ACCESSION BX255834
VERSION BX255834.1 GI:28411124
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Clarke, J.H.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK

COMMENT AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. _3 denotes a sequence derived from the 3' end of the
transposon, _5 denotes a sequence derived from the 5' end of the
transposon. BBSRC GARNET, ATIS project
On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock
code: N112982.

FEATURES

Location/Qualifiers

JOURNAL

Submitted (06-APR-2001) Yang S., Department of Biological Sciences,
National University of Singapore, 119260, SINGAPORE
COMMENT On Apr 12, 2001 this sequence version replaced gi:11558276.
FEATURES Location/Qualifiers
source 1..1740
/organism="Dendrobium cv. 'Sonia'"
/mol_type="mRNA"
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/db_xref="GOA:Q9FE45"
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ORIGIN

Alignment Scores:
Pred. No.: 0.00481 Length: 1740
Score: 80.00 Matches: 14
Percent Similarity: 73.91% Conservative: 3
Best Local Similarity: 60.87% Mismatches: 6
Query Match: 54.42% Indels: 0
DB: 8 Gaps: 0

ORIGIN

US-10-014-101B-32 (1-28) x DSO294542 (1-1740)
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Db 1288 GGTCCAATACTGTTTATCCTACAAAAGATCAAAATGGGATAAAGGATGTCTACTTCA 1347
Qy 24 IleProGlu 26
Db 1348 ATCCAGAT 1356

RESULT 38
AY209184

LOCUS Hordeum vulgare cytokinin dehydrogenase 3 mRNA, complete cds.
DEFINITION Hordeum vulgare cytokinin dehydrogenase 3 mRNA, complete cds.
ACCESSION AY209184
VERSION AY209184.1 GI:28883583
KEYWORDS Hordeum vulgare
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

REFERENCE 1 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Cytokinin dehydrogenase genes in barley
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1866)
AUTHORS Galuszka, P. and Frebort, I.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Dept. of Biochemistry, University of
Palacky, Slechtitelu 11, Olomouc 78371, Czech Republic

FEATURES

Location/Qualifiers

Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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ORIGIN

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Query Match: 55.10% Indels: 0
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US-10-014-101B-32 (1-28) x AK101022 (1-1930)

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Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1405 TCGGTGGTGACGCCGGAGGAGAC 1428

RESULT 35

AX339733
LOCUS AX339733 1515 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 30 from Patent WO0196580.
ACCESSION AX339733
VERSION AX339733.1 GI:18135726
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Schmuelling,T. and Werner,T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 0196580-A 30 20-DEC-2001;
JOURNAL Schmuelling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity: 46.15% Mismatches: 5
Query Match: 54.42% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX339733 (1-1515)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1150 ACAAGCAACGGCCCGTCTACCGAGTGAACAAATCAAATGGGACAAATCAAACA 1209

Qy 21 SerAlaMetIleProGlu 26
Db 1210 TCAGCAGTAACACCGGAG 1227
RESULT 36
AX785081
LOCUS AX785081 1515 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 30 from Patent WO03050287.
ACCESSION AX785081
VERSION AX785081.1 GI:32952912
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 Schmullling,T. and Werner,T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 03050287-A 30 19-JUN-2003;
JOURNAL Schmullling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES Location/Qualifiers
source 1. .1515
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/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 0.0041 Length: 1515
Score: 80.00 Matches: 12
Percent Similarity: 80.77% Conservative: 9
Best Local Similarity: 46.15% Mismatches: 5
Query Match: 54.42% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX785081 (1-1515)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1150 ACAAGCAACGGCCCGTCTACCGAGTGAACAAATCAAATGGGACAAACA 1209
Qy 21 SerAlaMetIleProGlu 26
Db 1210 TCAGCAGTAACACCGGAG 1227

RESULT 37

DSO294542
LOCUS DSO294542 1740 bp mRNA linear PLN 10-APR-2001
DEFINITION Dendrobium 'Sonia' mRNA for cytokinin oxidase (cko1 gene).
ACCESSION AJ294542
VERSION AJ294542.2 GI:13620164
KEYWORDS cko1 gene; cytokinin oxidase.
SOURCE Dendrobium cv. 'Sonia'
ORGANISM Dendrobium cv. 'Sonia'
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; higher Epidendroideae; Dendrobleae; Dendrobiinae; Dendrobium.

REFERENCE 1

AUTHORS Yang,S., Yu,H. and Goh,C.
TITLE Molecular cloning and characterization of a cDNA encoding cytokinin oxidase in Dendrobium sonia orchid
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1740)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2000) Yang S., Department of Biological Sciences, National University of Singapore, 119260, SINGAPORE
REMARK revised by [3]
REFERENCE 3 (bases 1 to 1740)
AUTHORS Yang,S.
TITLE Direct Submission

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/number=5
exon complement (12108. .12224)
/gene="AT4g29440"
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gene 13488. .17277
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15361. .15432,15515. .15722,15808. .16848,17202. .17277))
/gene="AT4g29450"
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Contains Protein kinases signatures and profile
AA572-594;Protein kinases signatures and profile AA698-710
contains EST gb:Z37592"
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Alignment Scores:					
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Score:	83.00	Matches:	19		
Percent Similarity:	37.93%	Conservative:	3		
Best Local Similarity:	32.76%	Mismatches:	6		
Query Match:	56.46%	Indels:	30		
DB:	8	Gaps:	1		

US-10-014-101B-32 (1-28) x ATCHRIV71 (1-200001)

Qy	1	SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys-----	15
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Qy	15	-----	15

Db	103418	TGATTTGTTTATTGAAAGTATATCCCAATAATGTATGTTAAATTGTTAACAGATT	103477
Qy	16	-----TrpAspAsnArgMetSerAlaMetileProGluileAsp 28	
Db	103478	TATTTTATTATAGATGGAACAACCGCATGTCAACGATGACACCGGACGAAGAT	103531

RESULT 34
AK101022
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023149Q03, full insert sequence.
ACCESSION AK101022
VERSION AK101022.1 GI:32986231
KEYWORDS FLI_CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN: Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764

2 (bases 1 to 1930)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Kato,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koda,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Kato,H., Kawai,J.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

AUTHORS	Rose,M., Hempel,S., Entian,K.-D., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
JOURNAL	Unpublished
REFERENCE	3 (bases 110074 to 200000)
AUTHORS	Zimmermann,W., Grueneisen,A., Wambutt,R., Kalicki,J., Wohldmann,P., Smith,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
JOURNAL	Unpublished
REFERENCE	4 (bases 1 to 200001)
AUTHORS	EU Arabidopsis sequencing,project.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV70 at the 5' end and an overlap with ATCHRIV72 at the 3' end.
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	/number=1
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intron    1813. 1907
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intron    2758. 2864
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          /number=7
intron    2981. 3070
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          /number=8
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exon      3383. 3588
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CDS       complement(join(3892. 4080,4202. 4333,4424. 4501,
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Alignment Scores:
Pred. No.:      0.141      Length:      88011
Score:          83.00      Matches:     19
Percent Similarity: 37.93%      Conservative: 3
Best Local Similarity: 32.76%      Mismatches: 6
Query Match:     56.46%      Indels:    30
DB:              8          Gaps:      1
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US-10-014-101B-32 (1-28) x ATT16L4 (1-88011)

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Qy      1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
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Db      78543 TCAACTTCTGGTGTACTCTCTCTATCCACAAACGAAATATTTACTTTT 78602

Qy      15 ----- 15

Db      78603 TGATTTTGTTTTATTGAAAGTATATCCCAATAATGTATGTTAAATTTAACAAGAAATT 78662

Qy      16 -----TrrAspAsnArgMetSerAlaMetIleProGluIleAsp 28
      |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      78663 TATTTTATTAAATAGATGGAACAACCGCATGTCAACGATGACACCGGACGAAGAT 78716
```

```
RESULT 33
ATCHRIV71
LOCUS      ATCHRIV71      200001 bp      DNA      linear      PLN 16-MAR-2000
DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 71.
ACCESSION  AL161575
VERSION     AL161575.2      GI:7269840
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 24920)
AUTHORS    Lennard,N., Quail,M., Harris,B., Rajandream,M.A., Barrell,B.G.,
            Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
JOURNAL     Unpublished
REFERENCE   2 (bases 24816 to 112826)
```


QY 16 -----TtpAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2477 TATTTTATTAGATGGACAACCGCATGTCAACGATGACACCGGACGAAGAT 2530
RESULT 31
AX785058 LOCUS AX785058 2782 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 7 from Patent WO03050287.
ACCESSION AX785058
VERSION AX785058.1 GI:32952892
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
Schmullling,T. and Werner,T.
Method for modifying plant morphology, biochemistry and physiology
Patent: WO 03050287-A 7 19-JUN-2003;
Schmullling, Thomas (DE) ; Werner, Tomas (DE)
Location/Qualifiers
1. .2782
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN
Alignment Scores:
Pred. No.: 0.00261 Length: 2782
Score: 83.00 Matches: 19
Percent Similarity: 37.93% Conservative: 3
Best Local Similarity: 32.76% Mismatches: 6
Query Match: 56.46% Indels: 30
DB: 6 Gaps: 1
US-10-014-101B-32 (1-28) x AX785058 (1-2782)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2357 TCAACTTCTGGTGTTACTCTCTTCTATCCACAACCGAACAAGTAATATTACITTT 2416
QY 15 ----- 15
Db 2417 TGATTTTGTTTTATTGTGAAGTATATCCCAATAATGTATGTTAAATTGTTAACAAGATT 2476
QY 16 -----TtpAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2477 TATTTTATTAGATGGACAACCGCATGTCAACGATGACACCGGACGAAGAT 2530
RESULT 32
ATT16L4
LOCUS Arabidopsis thaliana 88011 bp DNA linear PLN 17-JUN-1999
DEFINITION Arabidopsis thaliana DNA chromosome 4, BAC clone T16L4 (ESSA project).
ACCESSION AL079344
VERSION AL079344.1 GI:5123543
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
Bevan,M., Rose,M., Hempel,S., Entian,K.-D., Bancroft,I.,
Mewes,H.W., Mayer,K.F.X., Lemcke,K. and Schueller,C.
Unpublished
2 (bases 1 to 88011)
EU Arabidopsis sequencing,project.
Direct Submission
Submitted (17-JUN-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
schueller@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
1. .88011
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia"
/db_xref="taxon:3702"
/chromosome="4"
47. .1157
/gene="T16L4.10"
join(<47. .117,312. .365,446. .551,648. .716,803. .946, 1056. .1157)
/gene="T16L4.10"
/note="similarity to X-Pro dipeptidase, Homo sapiens, PIR2:A32454"
/codon_start=1
/product="X-Pro dipeptidase-like protein (fragment)"
/protein_id="CAB45310.1"
/db_xref="GI:5123544"
/db_xref="GOA:Q9SU95"
/db_xref="UniProt/TREMBL:Q9SU95"
/translation="AVLDAHNSVISAMKPGVNWVDMHKLAEKILESILKKGSIITGDDV DMMVQLGAVFMPHGLGHFMGIDTDTGGYPKGVPRPKPKGLSLRTARDLLLEGMMVI TVEPGCYFIKALLFPAMANATTSKFENRETIERFRNFGGVRIESDLVVVTANGCKNMTN VPRETWEIEAVMAGGPWPPTK"
47. .117
/gene="T16L4.10"
/number=1
118. .311
/gene="T16L4.10"
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312. .365
/gene="T16L4.10"
/number=2
366. .445
/gene="T16L4.10"
/number=2
446. .551
/gene="T16L4.10"
/number=3
552. .647
/gene="T16L4.10"
/number=3
648. .716
/gene="T16L4.10"
/number=4
717. .802
/gene="T16L4.10"
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803. .946
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/number=5
947. .1055
/gene="T16L4.10"
/number=5
1056. .1157
/gene="T16L4.10"
/number=6
1575. .3588
/gene="T16L4.20"
join(1575. .1812,1908. .1918,2041. .2196,2293. .2356, 2437. .2579,2670. .2757,2865. .2980,3071. .3221,3383. .3588)
/gene="T16L4.20"
/note="contains EST gb:H37349, T45910, H37681, Z26403, AA041059"
/codon_start=1
/product="arginine methyltransferase (pam1)"
/protein_id="CAB45311.1"


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source
1. .1677
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN
Alignment Scores:
Pred. No.: 0.000312 Length: 1677
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservative: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 6

US-10-014-101B-32 (1-28) x AX653630 (1-1677)

Qy 2 AlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
Db 1318 GCCATGGGCCCGTCTCATCTACCCCATGAACCGCAACAGTGGGACAGTAACATGTGCG 1377

Qy 22 AlaMetIleProGluIleAsp 28
Db 1378 GCAGTGATCACCGACGACGAC 1398

RESULT 26
AJ606944 2146 bp mRNA linear PLN 14-APR-2004
LOCUS
DEFINITION Zea mays mRNA for cytokinin oxidase 3 (cko3 gene), clone 2.
ACCESSION AJ606944
VERSION AJ606944.1 GI:38520864
KEYWORDS cko3 gene; cytokinin oxidase 3.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Massonneau,A., Houba-Herin,N., Pethe,C., Madzak,C., Majira,A.,
Falque,M., Rogowsky,P. and Laloue,M.
TITLE Differential expression of cytokinin oxidase genes in maize
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2146)
AUTHORS Houba-Herin,N.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Houba-Herin N., Biologie Cellulaire, Inra,
Route de St Cyr, Versailles cedex, 78026, FRANCE

FEATURES
source
1. .2146
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/chromosome="8"
/map="88.17-145.93 cm"
/clone="2"
/tissue_type="kernel"
/note="BIN 8.06"
1. .2146
/gene="cko3"
68. .1645
/gene="cko3"
/codon_start=1
/product="cytokinin oxidase 3"
/protein_id="CAE55202.1"
/db_xref="GI:38520865"
/translation="MKPPSSLVHYFKLLVLLALARLTMHVPDEDVLLSLGALRLDGHF
SFHDVSAAMARDFGNQCSFLPAAVLHPGSVSDIAIVRHVFSLGECSPLTVAARGHGH
LMQGSQAAGIIVRMESLRGRLQVNDAGVSPPSVDAPGSELWINVLRETLKHGLAPK
SWTDYHLHTVGGTLSNAGVQAFRHGPQVSNVQLIEIVTGRGDVVTCSPPDDNADLFY
AALGDLGQFGIITRIARIALEPAPKMWIRVLVLYSDFESFTEDQEMLIMAENSFYVEG
FVILNRTGVLNNWRASFQDPVPEASHFQSDGRVLYCLELTKNFNSDDTDTTMEQEVTV
LLSRLRFIQSTLFHTDVTYLEFLDRVHTSELKLRQAQWVPHPWLNLLIPRSIRRF
AKEVFGKILKDSNPGIILYFVNKSKWDNRTSVVPDEEIFYLVGFLSSAPSLSYGS
IAHSMNLNKQIIVEFCEEAGIGMKQYLAPYTTQQQWKAHFGARWETFERRKHYDPLAI
```

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ORIGIN
LAPGQRIFPKASLPLPL"

Alignment Scores:
Pred. No.: 0.00061 Length: 2146
Score: 86.00 Matches: 15
Percent Similarity: 76.92% Conservative: 5
Best Local Similarity: 57.69% Mismatches: 6
Query Match: 58.50% Indels: 0
DB: 8

US-10-014-101B-32 (1-28) x AJ606944 (1-2146)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1277 AGCAACAATGGTCCCATATGTCTTATCCAGTGAACAAATCAAAGTGGGACACAGAAGC 1336

Qy 21 SerAlaMetIleProGlu 26
Db 1337 TCAGTAGTCATACCCAGAT 1354

RESULT 27
AX653027 1587 bp DNA linear PAT 22-MAR-2003
LOCUS
DEFINITION Sequence 2897 from Patent WO03000898.
ACCESSION AX653027
VERSION AX653027.1 GI:29155841
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 2897 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
source
1. .1587
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN

Alignment Scores:
Pred. No.: 0.000633 Length: 1587
Score: 85.00 Matches: 14
Percent Similarity: 80.00% Conservative: 6
Best Local Similarity: 56.00% Mismatches: 5
Query Match: 57.82% Indels: 0
DB: 6

US-10-014-101B-32 (1-28) x AX653027 (1-1587)

Qy 4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
Db 1255 GGCCTCATCTCATGTACCCCATGAATAAGGACATGTGGGATGACAGGATGACGGCGATG 1314

Qy 24 IleProGluIleAsp 28
Db 1315 ACGCCGACGAGGAC 1329

RESULT 28
AX654568 1566 bp DNA linear PAT 22-MAR-2003
LOCUS
DEFINITION Sequence 4438 from Patent WO03000898.
ACCESSION AX654568
VERSION AX654568.1 GI:29157382
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
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Db	1282	TCAGTGGTCATACCAGAT	1299	
RESULT 24				
AK121317				
LOCUS	AK121317	2328 bp	mrna	linear
DEFINITION	Oryza sativa (japonica cultivar-group)	cdna clone:J023113D01, full insert sequence.	PLN 29-OCT-2003	
ACCESSION	AK121317.1	GI:37990940		
VERSION	FLI_CDNA; CAP trapper.			
KEYWORDS	Oryza sativa (japonica cultivar-group)			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
REFERENCE	1			
AUTHORS	The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohta,Y., Otsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ootomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN: Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M., and Hayashizaki,Y.			
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice			
JOURNAL	Science	301 (5631),	376-379	(2003)
MEDLINE	22752273			
PUBMED	12869764			
REFERENCE	2			
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koda,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakahama,Y., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.			
TITLE	Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice			
JOURNAL	Unpublished			
REFERENCE	3	(bases 1 to 2328)		
AUTHORS	Kikuchi,S.			
TITLE	Direct Submission			
JOURNAL	Submitted (31-JAN-2003)	Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)		
COMMENT	This clone is one of the 32K full-length cDNA clones from japonica rice.			
URL	http://cdna01.dna.affrc.go.jp/cDNA/NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Yamamoto,M. and Nakahama,Y.			
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.				
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Katoh,H., Kawai,J., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kouda,M., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.				
FEATURES	Location/Qualifiers			
source	1..2328			
organism	"Oryza sativa (japonica cultivar-group)"			
mol_type	"mrna"			
cultivar	"Nipponbare"			
db_xref	"taxon:39947"			
clone	"J023113D01"			
ORIGIN				
Alignment Scores:				
Pred. No.:	0.000311	Length:	2328	
Score:	88.00	Matches:	16	
Percent Similarity:	73.08%	Conservative:	3	
Best Local Similarity:	61.54%	Mismatches:	7	
Query Match:	59.86%	Indels:	0	
DB:	8	Gaps:	0	
US-10-014-101B-32 (1-28) x AK121317 (1-2328)				
QY	1	SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet	20	
Db	1449	AGCAACAATGGTCCCATACTGCTTTACCCAGTGAACAGAACCAAGTGGGACACAGACA	1508	
QY	21	SerAlaMetIleProGlu	26	
Db	1509	TCAGTGGTCATACCAGAT	1526	
RESULT 25				
AX653630				
LOCUS	AX653630	1677 bp	DNA	linear
DEFINITION	Sequence	3500 from Patent WO03000898.		
ACCESSION	AX653630			
VERSION	AX653630.1	GI:29156444		
KEYWORDS	Oryza sativa			
SOURCE	Oryza sativa			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
REFERENCE	1			
AUTHORS	Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M., Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.			
TITLE	Plant genes involved in defense against pathogens			
JOURNAL	Patent: WO 03000898-A 3500 03-JAN-2003; Syngenta Participations AG (CH)			
FEATURES	Location/Qualifiers			


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/codon_start=1
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/protein_id="AAG30906.1"
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AGKLTSSSSVESAAATDFGVTIKIPPSAVLIPSSVEDITDLIKLSFDSQSPPLAARG
HGHSRRGQASAKDGVVVMRSMVNRDRGIKVSRCTLYVDVAWLWIEVLNKTLELGL
TPVSWTDYLYLTVGGTLSNGGISGQTFRYGPOITNVLEMDVITGKEIATCSKDMNSD
LFFAVLGGGLGQFGIITRAIKLEVAPKRAKWLRLYIDFSEFTRDQERVISKTDGVDF
LEGSIMVDHGPPDNRSTYPPPSDHLRIASMVKRHRVLYCLEVKKYDETSQYTVNEE
MEELSDSLNHVRGFMVEKDVTYMDFLNRVRTGELNLSKQGWDPHPWNLNLFVPKTI
SKFDDGVFKGIILRNNTISGPVLVYPMNRNKWNRMSAAIPEEDVFYAVGFLRSAGFD
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ILSPGQNIFQKINSS"
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ORIGIN

Alignment Scores:
Pred. No.: 9.11e-06 Length: 1572
Score: 96.00 Matches: 18
Percent Similarity: 80.77% Conservative: 3
Best Local Similarity: 69.23% Mismatches: 5
Query Match: 65.31% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x AF303979 (1-1572)

Qy 3 SerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAsnArgMetSerAla 22
Db 1231 AGCGGTCTGTTCTTGTATTATCCATGAATCGCAACAAGTGAATGATCGGATGTCGCC 1290
Qy 23 MetIleProGluIleAsp 28
Db 1291 GCTATACCGGAGGAAGAT 1308

RESULT 22
AJ606943
LOCUS AJ606943 2134 bp mRNA linear PLN 14-APR-2004
DEFINITION Zea mays mRNA for cytokinin oxidase 3 (cko3 gene), clone 1.
ACCESSION AJ606943
VERSION AJ606943.1 GI:38520862
KEYWORDS cko3 gene; cytokinin oxidase 3.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 Massonneau, A., Houba-Herlin, N., Pethe, C., Madzak, C., Majira, A.,
Falque, M., Rogowsky, P. and Laloue, M.
AUTHORS Differential expression of cytokinin oxidase genes in maize

TITLE Unpublished
JOURNAL (bases 1 to 2134)

AUTHORS Houba-Herlin, N.
TITLE Direct Submission

JOURNAL Submitted (17-NOV-2003) Houba-Herlin N., Biologie Cellulaire, Inra,
Route de St Cyr, Versailles cedex, 78026, FRANCE

FEATURES
source
1. .2134
/organism="Zea mays"
/mol_type="mRNA"
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CDS
1. .2134
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75. .1652
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LMGQSQAAQGIIVRMESLRGPRLQVNDGGVSPSDAPGGELWINVLRLELKHGLAPK
SWTDYHLHTVGGTLSNAGVSGQAFRHGPQVSNVQLEIVTGRGDVVTCSRDDNADLFY
AALGGLGQFGIITRAIALEPAPKMWIRVLYSDSFESFTEQEMLIAMENSFDYVEG
FVIINRTGVLNWRASFKPDQPVASHFQSDGRVLYCLELTKNFNSDDTDTTMEQEVTV
LLSRLRFIQSTLTFHTDVTYLEFLDRVHTSELKRAQGLWEVPHWNLNLI PRSSIRRF
AKEVFGKILKDSNNGPIILLYPVNRSKWDNRTSVVIPDEEIFYLVGFLSSAPLSGYGS
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ORIGIN

Alignment Scores:
Pred. No.: 0.000191 Length: 2134
Score: 89.00 Matches: 16
Percent Similarity: 76.92% Conservative: 4
Best Local Similarity: 61.54% Mismatches: 6
Query Match: 60.54% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x AJ606943 (1-2134)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAsnArgMet 20
Db 1284 AGCAACAATGGTCCCATATGCTTTATCCAGTGAACAGATCGAAGTGGACAACAGACG 1343
Qy 21 SerAlaMetIleProGlu 26
Db 1344 TCAGTAGTCATACCAGAT 1361

RESULT 23
AX653226
LOCUS AX653226 1590 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3096 from Patent WO03000898.
ACCESSION AX653226
VERSION AX653226.1 GI:29156040
KEYWORDS Oryza sativa
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
AUTHORS Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens

JOURNAL Patent: WO 03000898-A 3096 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES
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1. .1590
/organism="Oryza sativa"
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ORIGIN

Alignment Scores:
Pred. No.: 0.0002 Length: 1590
Score: 88.00 Matches: 16
Percent Similarity: 73.08% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 7
Query Match: 59.86% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX653226 (1-1590)

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Qy 21 SerAlaMetIleProGlu 26
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/ product="hypothetical protein"
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WNTGWTKSRGKKRIRINVYRPKIAPAKNKKPKPTKEQLMDPEFSDDELVLTSLGFDG
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9624. .9757
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/ codon_start=1
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FVVASDGTLAFHSLNSLVQSASFYSGKQDVMVAEPERVVRAHEGPAYDVKFYGED
EDALLSCGDDGRVRGWKREFAESDVS LHLKENHLKPLLELINPQHKGPWGALSPMP
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complement(17023. .17050)
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19827. .19874
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20755. .20797
/ rpt_family=" (TAAAAA)n"
complement(20851. .20873)
/ rpt_family="AT_rich"
21014. .24475
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LIRTDWFSSRSLRDWPLFMCCISLSIFPLAAFTVEKLV LQKYISEPVVIFLHIITM
TEVLYPVYVTLRCDSAFSLGVTMLLTCTI VWLKLVSYAHTSDIRSLANADKANPEV
SYVVSLSLAYFVMVAPTLCYQPSYPR SACIRKGVARQFAKLVIFTGEMGFIEQYIN
PIVRNSKHPLKGLLYAIERVLKLSVPNLVWLCMFYCF FHLWNLILAEILCFGDRF
YKDWNNAKSVGDYWRMNMVPVHKWVRHIYFPC LRSKIPKTLAIIIAFLVSAVFHEL
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complement(25990. .26015)
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26221. .26844
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26320. .26670
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/ db_xref="GI:4191776"
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SFKWIKDKCNKILN"
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/ rpt_family=" (CA)n"
complement(28356. .31273)
/ gene="At2g19470"
/ note="synonym: F3P11.7; supported by full length cDNA:
Ceres:2312"

Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGE (SSP) Consortium members constructed and sequenced the pENTR (ORF) clones using the RAFL cDNAs: Nguyen,M., Southwick,A., Tripp,M., Palm,C.J., Jones,T., Wu,T., Chen,H., Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toroumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

Location/Qualifiers

1. .1655
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AVDRGVSPVTWTDYLYLSVGGTSLNAGIGGQTFRHGPQISNVHELVDVITGKGMWTC
PKLNPELFYGVGLGQFGIITRARIADHAPTRVKSRLYSDFSAFKRDQERLISM
TNDLGVDFLEGQLMMSNGFVDTSPFPLSDQTRVASLVNDRHRIIYVLEVAKYYDRTILP
IIDQVIDTLRSLTGAPGFMFVQDVPYFDLNRVRNEEDKLRSLGLEWVPHWPLNIFV
PGSRIQDFHDGVINGLLNQTSTSGVTLFYPTNRKNWNRMTMTDDEDVFYVIGLLQ
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gene

CDS

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AARGQHSRLRGQASAPGVVNMTCCLAMAAKPAAVVISADGTADVAAGTMWVDVLA
AVDRGVSPVTWTDYLYLSVGGTSLNAGIGGQTFRHGPQISNVHELVDVITGKGMWTC
PKLNPELFYGVGLGQFGIITRARIADHAPTRVKSRLYSDFSAFKRDQERLISM
TNDLGVDFLEGQLMMSNGFVDTSPFPLSDQTRVASLVNDRHRIIYVLEVAKYYDRTILP
IIDQVIDTLRSLTGAPGFMFVQDVPYFDLNRVRNEEDKLRSLGLEWVPHWPLNIFV
PGSRIQDFHDGVINGLLNQTSTSGVTLFYPTNRKNWNRMTMTDDEDVFYVIGLLQ
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MFDPKRLLLSPGQDIFN"

ORIGIN

Alignment Scores:
Pred. No.: 9.57e-08 Length: 1655
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x BT000179 (1-1655)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyPrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTCTATCCCAACCGAAACAAATGGAACACCGCATG 1299

QY 21, SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAGAT 1323

RESULT 15

AY054460

LOCUS

DEFINITION Arabidopsis thaliana cytokinin oxidase-like protein (At4g29740;

T16L4.250) mRNA, complete cds.

ACCESSION

AY054460

VERSION AY054460.1 GI:15450760

KEYWORDS FLJ CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE

AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1863)

Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

Direct Submission

JOURNAL

Submitted (28-AUG-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT

e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : "RIKEN Arabidopsis Full-Length CDNA"): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGE (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

Location/Qualifiers

1. .1863
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="IV"
/clone="RAFL07-11-K12"
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1. .1863
/gene="At4g29740; T16L4.250"
89. .1663
/gene="At4g29740; T16L4.250"
/codon_start=1
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PGSRIQDFHDGVINGLLNQTSTSGVTLFYPTNRKNWNRMTMTDDEDVFYVIGLLQ
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gene

CDS

ORIGIN

Alignment Scores:
Pred. No.: 1.1e-07 Length: 1863
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x AY054460 (1-1863)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyPrProThrAsnArgAsnLysTrpAspAsnArgMet 20

Db 1328 TCAACTTCTGGTGTACTCTCTTCTATCCCAACCGAAACAAATGGAACACCGCATG 1387

Db 1240 TCAACTTCTGGTGTACTCTCTTCTATCCACAACCGAAACAATGGAACAACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28

Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 12

AX785079

LOCUS AX785079 1575 bp DNA linear PAT 17-JUL-2003

DEFINITION Sequence 28 from Patent WO03050287.

ACCESSION AX785079

VERSION AX785079.1 GI:32952910

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Schmulling, T. and Werner, T.

AUTHORS Method for modifying plant morphology, biochemistry and physiology

TITLE Patent: WO 03050287-A 28 19-JUN-2003;

JOURNAL Schmulling, Thomas (DE); Werner, Tomas (DE)

FEATURES

Location/Qualifiers

source 1. .1575

/organism="Arabidopsis thaliana"

/mol_type="unassigned DNA"

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ORIGIN

Alignment Scores:

Pred. No.: 9.04e-08 Length: 1575

Score: 108.00 Matches: 19

Percent Similarity: 78.57% Conservative: 3

Best Local Similarity: 67.86% Mismatches: 6

Query Match: 73.47% Indels: 0

DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX785079 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20

Db 1240 TCAACTTCTGGTGTACTCTCTTCTATCCACAACCGAAACAATGGAACAACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28

Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 13

AF303980

LOCUS AF303980 1575 bp mRNA linear PLN 08-NOV-2000

DEFINITION Arabidopsis thaliana cytokinin oxidase (CKX4) mRNA, complete cds.

ACCESSION AF303980

VERSION AF303980.1 GI:11120511

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1575)

AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.

TITLE A family of cytokinin oxidases from Arabidopsis thaliana

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1575)

AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.

TITLE Direct Submission

JOURNAL Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA

FEATURES

Location/Qualifiers

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/translation="MTNTLCLSLITLITFFISLTPTLIKSDGIDVFLPISLNLTVLTDPFSISAASHDFGNITDENPGAVLCPSTTEVARLLRFANGFGSYNKGSTSPASTFKVAARGQSHSLRQASAPGGVVNMTCCLMAAKPAAVVISADGTYADVAGTWWVDVLKAADRGVSPVTWTDLYLSVGGTSLNAGIGGQTFRHGQISNVHELDVITCKGEMMTCSPKLNPELFYVGLGQFGIITRARIALDHAPTRVKWSRILYSDFSFKRQDQERLISM TNDLGVDLFEGQLMMSNGFVDTSFPLSDQTRVASLVNDHRIIYVLEVAKYVDRTTLP IIDQVIDTSLRTGLFPAGFMFVQDVFDFLNRVRNEEDKLRSLGLWEVPHWLNIFV PGSRIQDFHGDVINGLLLNQTSVTLFYPYPTNRKNRMSTMTPDDEVFYVIGLLIQ SAGGSQNWQELNLDKVIQFCENSGIKIKEYLMHYTRKEDWVKHFGPKWDDFLRKKI MFDPKRLLSFGQDIFN"

ORIGIN

Alignment Scores:

Pred. No.: 9.04e-08 Length: 1575

Score: 108.00 Matches: 19

Percent Similarity: 78.57% Conservative: 3

Best Local Similarity: 67.86% Mismatches: 6

Query Match: 73.47% Indels: 0

DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x AF303980 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20

Db 1240 TCAACTTCTGGTGTACTCTCTTCTATCCACAACCGAAACAATGGAACAACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28

Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 14

BT000179

LOCUS BT000179 1655 bp mRNA linear PLN 19-SEP-2002

DEFINITION Arabidopsis thaliana cytokinin oxidase-like protein (At4g29740) mRNA, complete cds.

ACCESSION BT000179

VERSION BT000179.1 GI:23197941

KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1655)

AUTHORS Nguyen, M., Karlin-Neumann, G., Southwick, A., Tripp, M., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,

3'UTR SGLALLYPTNRNKNWNRMSAMPEIDEDVIYIIGLLQSATPKDLPEVESVNEKIIIRFC
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ORIGIN

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Pred. No.: 3e-14 Length: 1687
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x BT004107 (1-1687)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1225 TCAGCTTCGGGACTCGCTCTTCTATCCAAACCGGAATAAATGGGACAATCGTATG 1284

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1285 TCGGCGATGATACCAGAGATCGAT 1308

RESULT 9
AX339731
LOCUS AX339731 1575 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 28 from Patent WO0196580.
ACCESSION AX339731
VERSION AX339731.1 GI:18135724

KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Schmuelling,T. and Werner,T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 0196580-A 28 20-DEC-2001;
Schmuelling, Thomas (DE) ; Werner, Tomas (DE)
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/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 9.04e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservatave: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX339731 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTTCTATCCAAACCGGAACAAATGGAACACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 10
AX507394
LOCUS AX507394 1575 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2089 from Patent WO0216655.
ACCESSION AX507394
VERSION AX507394.1 GI:23388631
KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 2089 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 9.04e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservatave: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX507394 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTTCTATCCAAACCGGAACAAATGGAACACCGCATG 1299
Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 11
AX651615
LOCUS AX651615 1575 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 428 from Patent WO03000898.
ACCESSION AX651615
VERSION AX651615.1 GI:29154433
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 428 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
source
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/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 9.04e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservatave: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x AX651615 (1-1575)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20

The Salk, Stanford, PGEN (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEN) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEN) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

FEATURES source

Location/Qualifiers
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/clone="U20989"
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/note="This clone is in pUNI 51."

gene

CDS

1. .1537
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1. .1506
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/evidence=experimental
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/protein_id="AAO64073.1"
/db_xref="GI:28973497"
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SNGGIGGVFRNGPLVSNVLELDVITGKEMLTCSRQLNPELFYGLGLGQFGIITR
ARIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTS
FFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSYLPFGFISMH
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SGLALLYPTNRKWDNRMSAMPEIDEDVVIIGLQSATPKDLPEVESVNEKIIRFC
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/gene="At2g19500"

3' UTR

ORIGIN

Alignment Scores:
Pred. No.: 2.7e-14 Length: 1537
Score: 147.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-32 (1-28) x BT005653 (1-1537)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTyrAspAsnArgMet 20
Db 1171 TCAGCTTCGGACTCGCTCTCTCTATCCAAACCGGAATAATGGACAATCGTATG 1230
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1231 TCGCGATGATACACAGATCGAT 1254

RESULT 8
BT004107

LOCUS BT004107 1687 bp mRNA linear PLN 14-FEB-2003
DEFINITION Arabidopsis thaliana clone RAFL15-29-H04 (R20989) putative
cytokinin oxidase (At2g19500) mRNA, complete cds.
ACCESSION BT004107
VERSION BT004107.1 GI:28393415
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsais.

REFERENCE AUTHORS

1 (bases 1 to 1687)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsis Full Length cDNA Clones

JOURNAL

Unpublished

REFERENCE AUTHORS

2 (bases 1 to 1687)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission

JOURNAL

Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

COMMENT

The Salk, Stanford, PGEN (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEN) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEN) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

FEATURES source

Location/Qualifiers

1. .1687
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="2"
/clone="RAFL15-29-H04 (R20989)"
/ecotype="Columbia"
/note="This clone is in a modified pBluescript vector2 (lambda PS) as a BamHI/XhoI insert."

gene

5' UTR

CDS

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55. .1560
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/protein_id="AAO42130.1"
/db_xref="GI:28393416"

/translation="MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISA
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SNGGIGGVFRNGPLVSNVLELDVITGKEMLTCSRQLNPELFYGLGLGQFGIITR
ARIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTS
FFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSYLPFGFISMH
DVAYFDLNRVHVEENKLSRLGLWELPHLPWNLNLYVPKSRILDFHNGVVKDILLKQKSA

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 07:19:31 ; Search time 6601 Seconds
(without alignments)
205.536 Million cell updates/sec

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Perfect score: 147
Sequence: 1 SASGLALLYPTNRNKNWDRMSAMPEID 28

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	84	AX339734	AX339734 Sequence
2	147	100.0	84	AX785082	AX785082 Sequence
3	147	100.0	1506	CQ812637	CQ812637 Sequence
4	147	100.0	1506	AX339729	AX339729 Sequence

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7	147	100.0	1537	8	BT005653	BT005653 Arabidops
8	147	100.0	1687	8	BT004107	BT004107 Arabidops
9	108	73.5	1575	6	AX339731	AX339731 Sequence
10	108	73.5	1575	6	AX507394	AX507394 Sequence
11	108	73.5	1575	6	AX651615	AX651615 Sequence
12	108	73.5	1575	6	AX785079	AX785079 Sequence
13	108	73.5	1575	8	AF303980	AF303980 Arabidops
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23	88	59.9	1590	6	AX653226	AX653226 Sequence
24	88	59.9	2328	8	AK121317	AK121317 Oryza sat
25	87	59.2	1677	6	AX653630	AX653630 Sequence
26	86	58.5	2146	8	AJ606944	AJ606944 Zea mays
27	85	57.8	1587	6	AX653027	AX653027 Sequence
28	83	56.5	1566	6	AX654568	AX654568 Sequence
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ALIGNMENTS

RESULT 1	AX339734	Sequence 31 from Patent WO0196580.	84 bp	DNA	linear	PAT 10-JAN-2002
LOCUS	AX339734	AX339734				
DEFINITION	AX339734	AX339734				
ACCESSION	AX339734	AX339734				
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SOURCE	Arabisopsis thaliana					
ORGANISM	Arabisopsis thaliana					
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REFERENCE	1	Schmuelling,T. and Werner,T.				
AUTHORS		Method for modifying plant morphology, biochemistry and physiology				
TITLE		Patent: WO 0196580-A 31 20-DEC-2001;				
JOURNAL		Schmuelling, Thomas (DE) ; Werner, Tomas (DE)				
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Percent Similarity:						

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RA Bilyeu K.D., Laskey J.G., Riekhof W.R., VanVickle S., Morris R.O.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF303982; AAG30909.1; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; I.
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SQ SEQUENCE 540 AA; 60389 MW; D74DD0D50CEBA76F CRC64;

Query Match      52.4%; Score 77; DB 2; Length 540;
Best Local Similarity 54.2%; Pred. No. 0.0069;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      3 SGLALLYPTNRNKKWDNRMSAMIP E 26
      |||::|||::|||::|||::|:
Db      409 SGPILYIPMNKDKWDRSSAVTPD 432

Search completed: February 22, 2005, 22:44:15
Job time : 179 secs
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ID Q8S0F8 PRELIMINARY; PRT; 525 AA.
AC Q8S0F8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative cytochrome oxidase.
GN Name=B1150F11.19;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Itonuma A., Iijima A., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316(2002).
DR EMBL; AP003412; BAB90259.1; -.
DR Gramene; Q8S0F8; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD binding_4; 1.
DR PROSITE; PS00862; OX2 COVAL_FAD; UNKNOWN 1.
SQ SEQUENCE 525 AA; 58011 MW; D10B03BFD4259DDD CRC64;

Query Match 59.9%; Score 88; DB 2; Length 525;
Best Local Similarity 61.5%; Pred. No. 0.00015;
Matches 16; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAMPIE 26
Db 404 SNNGPILLYPVNRTKWDNRRTSVVIPD 429

RESULT 6
Q94IV9
ID Q94IV9 PRELIMINARY; PRT; 558 AA.
AC Q94IV9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative cytochrome oxidase.
GN Name=P0419B01.11; Synonyms=B1046G12.5;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Itonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316(2002).
DR EMBL; AP003244; BAB56095.1; -.
DR EMBL; AP003200; BAB89407.1; -.
DR Gramene; Q94IV9; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR Pfam; PF01565; FAD binding_4; 1.
SQ SEQUENCE 558 AA; 59121 MW; B3472B591AD1EFF7 CRC64;

Query Match 59.2%; Score 87; DB 2; Length 558;
Best Local Similarity 59.3%; Pred. No. 0.00022;
Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ASGLALLYPTNRNKNWDRMSAMPIE 28
Db 440 AMGPVLIYPMNRNKNWDRMSAMITDDD 466

RESULT 7
Q709Q3
ID Q709Q3 PRELIMINARY; PRT; 525 AA.
AC Q709Q3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase 3.
GN Name=cko3;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kernel;
RA Massonneau A., Houba-Herlin N., Pethe C., Madzak C., Majira A.,
RA Falque M., Rogowsky P., Laloue M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ606944; CAE55202.1; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD binding_4; 1.
DR PROSITE; PS00862; OX2 COVAL_FAD; UNKNOWN 1.
SQ SEQUENCE 525 AA; 58504 MW; 56A43E6B255ECD6E CRC64;

Query Match 58.5%; Score 86; DB 2; Length 525;
Best Local Similarity 57.7%; Pred. No. 0.00029;
Matches 15; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAMPIE 26
Db 404 SNNGPILLYPVNKNWDRNRTSVVIPD 429

RESULT 8
Q709Q5
ID Q709Q5 PRELIMINARY; PRT; 519 AA.
AC Q709Q5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase 2.
GN Name=cko2;
OS Zea mays (Maize).


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DR EMBL; AL079344; CAB45334.1; --
DR EMBL; AL161575; CAB79732.1; --
DR EMBL; AY054460; AAK96652.1; --
DR EMBL; BT000179; AAN15498.1; --
DR PIR; T09937; T09937.
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; FALSE NEG.
KW Alternative splicing; FAD; Flavoprotein; Glycoprotein;
KW Multigene family; Oxidoreductase; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 524 Cytokinin dehydrogenase 4.
FT MOD_RES 109 109 Tele-8alpha-FAD histidine (By
similarity).
FT CARBOHYD 39 39 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 58 58 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 124 124 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 411 411 N-linked (GlcNAc... ) (Potential).
FT CONFLICT 15 15 L -> F (in Ref. 1).
SQ SEQUENCE 524 AA; 58061 MW; DBD23A7876DDA171 CRC64;

Query Match
Best Local Similarity 73.5%; Score 108; DB 1; Length 524;
Matches 19; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 SASGLALYPTRNRKWDNRMSAMPEID 28
|||:|||||:|||||:|
Db 414 STSGVTLFYPTNRKWNRMSTMTDDED 441

RESULT 3
CKX3_ARATH
ID CKX3_ARATH STANDARD; PRT; 523 AA.
AC Q9LTS3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cytokinin dehydrogenase 3 precursor (EC 1.5.99.12) (Cytokinin oxidase
3) (CKO 3).
GN Name=CKX3; OrderedLocusNames=At5G56970; ORFNames=MHM17.8;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21068113; PubMed=11154345; DOI=10.1104/pp.125.1.378;
RA Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,
RA Kramer M.D., Morris R.O.;
RT "Molecular and biochemical characterization of a cytokinin oxidase
from maize.";
RL Plant Physiol. 125:378-386(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
features of the regions of 3,076,755 bp covered by sixty P1 and TAC
clones.";
RL DNA Res. 7:31-63(2000).
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
CC substituted adenine derivatives that are plant hormones, where the
CC substituent is an isopentenyl group.
CC -!- CATALYTIC ACTIVITY: N(6)-dimethylallyladenine + acceptor + H(2)O =
CC adenine + 3-methylbut-2-enal + reduced acceptor.
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
```

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CC -----
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CC -----
DR EMBL; AF303979; AAG30906.1; --
DR EMBL; AB024035; BAA97027.1; --
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW FAD; Flavoprotein; Glycoprotein; Multigene family; Oxidoreductase;
KW Signal.
FT SIGNAL 1 31 Potential.
FT CHAIN 32 523 Cytokinin dehydrogenase 3.
FT MOD_RES 105 105 Tele-8alpha-FAD histidine (By
similarity).
FT CARBOHYD 153 153 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 408 408 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 523 AA; 59422 MW; 2324EBFC21D7103A CRC64;

Query Match
Best Local Similarity 65.3%; Score 96; DB 1; Length 523;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 SGLALLYPTNRNKWDNRMSAMPEID 28
|||:|||||:|||||:|
Db 411 SGPVLVYPMNRNKWDNRMSAAIPEED 436

RESULT 4
Q709Q4
ID Q709Q4 PRELIMINARY; PRT; 525 AA.
AC Q709Q4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytokinin oxidase 3.
GN Name=cko3;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kernel;
RA Massonneau A., Houba-Herlin N., Pethe C., Madzak C., Majira A.,
RA Falque M., Rogowsky P., Laloue M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ606943; CAE55201.1; --
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; UNKNOWN 1.
SQ SEQUENCE 525 AA; 58494 MW; 017201BBA5130F49 CRC64;

Query Match
Best Local Similarity 60.5%; Score 89; DB 2; Length 525;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SASGLALLYPTNRNKWDNRMSAMPE 26
|||:|||||:|||||:|
Db 404 SNNGPILLYPVNRSKWDNRSTSVIPD 429

RESULT 5
Q8S0F8
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF303978; AAG30905.1; --
DR EMBL; AC005917; AAD10149.2; --
DR InterPro; IPR006094; Oxid_FAD_bind_N.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW FAD; Flavoprotein; Glycoprotein; Multigene family; Oxidoreductase;
KW Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 501 Cytokinin dehydrogenase 2.
FT MOD_RES 92 92 Tele-8alpha-FAD histidine (By
FT similarity).
FT CARBOHYD 32 32 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 51 51 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 107 107 N-linked (GlcNAc . .) (Potential).
FT CONFLICT 157 157 G -> R (in Ref. 1).
SQ SEQUENCE 501 AA; 55583 MW; 9F8F0AAEAA4DE84A CRC64;

Query Match 100.0%; Score 147; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASGLALYPTRNKWDNRMSAMPEID 28
Db |||||
391 SASGLALYPTRNKWDNRMSAMPEID 418

RESULT 2
CKX4 ARATH STANDARD; PRT; 524 AA.
ID CKX4 ARATH STANDARD; PRT; 524 AA.
AC Q9FUJ2; Q9SU77;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cytokinin dehydrogenase 4 precursor (EC 1.5.99.12) (Cytokinin oxidase
DE 4) (CKO 4).
GN Name=CKX4; OrderedLocusNames=At4g29740; ORFNames=T16L4.250;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21068113; PubMed=11154345; DOI=10.1104/pp.125.1.378;
RA Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,
RA Kramer M.D., Morris R.O.;
RT "Molecular and biochemical characterization of a cytokinin oxidase
RT from maize."
RL Plant Physiol. 125:378-386 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,

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RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang B., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome."
RL Science 302:842-846 (2003).
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
CC substituted adenine derivatives that are plant hormones, where the
CC substituent is an isopentenyl group.
CC -!- CATALYTIC ACTIVITY: N(6)-dimethylallylamine + acceptor + H(2)O =
CC adenine + 3-methylbut-2-enal + reduced acceptor.
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. According to EST
CC sequences;
CC Name=1;
CC IsoId=Q9FUJ2-1; Sequence=Displayed;
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
CC -----
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DR

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OM protein - protein search, using sw model

Run on: February 22, 2005, 22:23:01 ; Search time 177 Seconds
(without alignments)
81.007 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRNKWDNRMSAMIPED 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	501	1 CKX2_ARATH	Q9fuj3 arabidopsis
2	108	73.5	524	1 CKX4_ARATH	Q9fuj2 arabidopsis
3	96	65.3	523	1 CKX3_ARATH	Q9lts3 arabidopsis
4	89	60.5	525	2 Q709Q4	Q709g4 zea mays (m
5	88	59.9	525	2 Q8S0F8	Q8s0f8 oryza sativ
6	87	59.2	558	2 Q94IV9	Q94iv9 oryza sativ
7	86	58.5	525	2 Q709Q3	Q709q3 zea mays (m
8	83	56.5	519	2 Q709Q5	Q709q5 zea mays (m
9	83	56.5	521	2 Q75K78	Q75k78 oryza sativ
10	80	54.4	504	2 Q9LY71	Q9ly71 arabidopsis
11	80	54.4	536	2 Q9FE45	Q9fe45 dendrobium
12	79	53.7	520	2 Q84U27	Q84u27 hordeum vul
13	77	52.4	512	2 Q9FWT3	Q9fwt3 arabidopsis
14	77	52.4	540	2 Q67YU0	Q67yu0 arabidopsis
15	77	52.4	540	2 Q9FUJ0	Q9fuj0 arabidopsis
16	75	51.0	526	2 Q8S394	Q8s394 hordeum vul
17	75	51.0	526	2 Q8H6F6	Q8h6f6 hordeum vul
18	75	51.0	527	2 Q6YW51	Q6yw51 oryza sativ
19	74	50.3	532	1 CKX1_ORYSA	Q9ide6 oryza sativ
20	70	47.6	241	2 Q6QJL4	Q6qjl4 fagopyrum e
21	69	46.9	524	2 Q9FUJ1	Q9fuj1 arabidopsis
22	68	46.3	137	2 Q94KI1	Q94ki1 hordeum vul
23	68	46.3	137	2 Q94KI5	Q94ki5 triticum ae
24	68	46.3	527	2 Q8LNV6	Q8lnv6 oryza sativ
25	63	42.9	534	1 CKX1_MAIZE	Q9t0n8 zea mays (m
26	62	42.2	524	2 Q6YW50	Q6yw50 oryza sativ
27	58	39.5	575	2 O22213	O22213 arabidopsis
28	57	38.8	532	2 Q7XKG2	Q7xkg2 oryza sativ
29	56	38.1	222	2 Q6LGW6	Q6lgw6 photobacter
30	56	38.1	1274	1 NPC2_CAEEL	P34389 caenorhabdi
31	55	37.4	120	2 Q8R9F1	Q8r9f1 thermoanaer

RESULT 1

ID	CKX2_ARATH	STANDARD;	PRT;	501 AA.
AC	Q9FUJ3; Q9ZUP1;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cytokinin dehydrogenase 2 precursor (EC 1.5.99.12) (Cytokinin oxidase 2) (CKO 2).			
GN	Name=CKX2; OrderedLocusNames=At2g19500; ORFNames=F3P11.10;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsiis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21068113; PubMed=11154345; DOI=10.1104/pp.125.1.378;			
RA	Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,			
RA	Kramer M.D., Morris R.O.;			
RT	"Molecular and biochemical characterization of a cytokinin oxidase from maize."			
RT	Plant Physiol. 125:378-386(2001).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=cv. Columbia;			
RC	MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;			
RX	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,			
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,			
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,			
RA	Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,			
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,			
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,			
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,			
RA	Venter J.C.;			
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."			
RT	Nature 402:761-768(1999).			
RL				
CC	-!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-substituted adenine derivatives that are plant hormones, where the substituent is an isopentenyl group.			
CC	-!- CATALYTIC ACTIVITY: N(6)-dimethylallyladenine + acceptor + H(2)O = adenine + 3-methylbut-2-enal + reduced acceptor.			
CC	-!- COFACTOR: FAD (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Extracellular.			
CC	-!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked oxidoreductase family.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/			

RESULT 12
AG3612
glycerol kinase (EC 2.7.1.30) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3612
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letese
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3612
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-356 <KUR>
A;Cross-references: UNIPROT:Q8YBR2; GB:AE008918; PIDN:AAL54066.1; PID:g17985022; GSPDB:G
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10824
A;Map position: 11
C;Keywords: phosphotransferase

Query Match 35.0%; Score 51.5; DB 2; Length 356;
Best Local Similarity 32.1%; Pred. No. 5.3;
Matches 9; Conservative 7; Mismatches 5; Indels 7; Gaps 1;

QY 7 LLYPTNRNKKWDNRN-----SAMIPEI 27
||| ||| : : : : :
Db 47 LIYHIGENRWDELLDILGIPAAMLPEV 74

RESULT 13
T04332
glutamate-cysteine ligase (EC 6.3.2.2) - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04332
R;Kovari, I.A.; Goldsbrough, P.B.
submitted to the EMBL Data Library, August 1997
A;Description: Tomato GSH1 cDNA coding for gamma-glutamylcysteine synthetase.
A;Reference number: Z15289
A;Accession: T04332
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-523 <KOV>
A;Cross-references: UNIPROT:O22493; EMBL:AF017983; PIDN:AAB71230.1; PID:g2
A;Experimental source: strain Ohio State 4
C;Genetics:
A;Gene: GSH1
C;Keywords: ligase

Query Match 33.7%; Score 49.5; DB 2; Length 523;
Best Local Similarity 42.1%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 9 YPTNRNKKWDNRNMSAMIPEI 27
||| ||| : : : : :
Db 370 YPT-LNDWENHLTTFPEV 387

RESULT 14
H69824
hypothetical protein yhdB - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69824
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69824
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-80 <KUN>
A;Cross-references: UNIPROT:O07530; GB:Z99108; GB:Z99109; GB:AL009126; NID:g2633260; FI
A;Experimental source: strain 168
C;Genetics:
A;Gene: yhdB

Query Match 33.3%; Score 49; DB 2; Length 80;
Best Local Similarity 47.1%; Pred. No. 2.4;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 8 LYPTNRNKKWDNRMSAMI 24
||| ||| : : : : :
Db 10 LYTHRSQWDNLLILMV 26

RESULT 15
E82099
phosphatidate cytidyltransferase VC2255 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82099
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <HEI>
A;Cross-references: UNIPROT:Q9KPV7; GB:AE004297; GB:AE003852; NID:g9656810; PIDN:AAF953
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2255
A;Map position: 1
C;Superfamily: phosphatidate cytidyltransferase

Query Match 33.3%; Score 49; DB 2; Length 280;
Best Local Similarity 47.1%; Pred. No. 9.7;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 ASGLALLYPTNRNKKWDN 18
: ||| : || : || : :
Db 97 SSGLAITYPRSRPLWEH 113

Search completed: February 22, 2005, 22:45:00
Job time : 41 secs

R.;Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84842
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-575 <STO>
A;Cross-references: GB:AE002093; NID:g2618686; PIDN:AAB84333.1; GSPDB:GN00139
C;Genetics:
A;Gene: T32G6.3; At2g41510
A;Map position: 2
A;Introns: 223/1; 265/3; 352/3; 440/2
C;Superfamily: poppy reticuline oxidase

Query Match 39.5%; Score 58; DB 2; Length 575;
Best Local Similarity 38.5%; Pred. No. 0.92;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 3 SGLALLYPTNRNKNWDRMSAMIPEID 28
Db 428 NGPILYPVNSQSKWKHTSLTPNED 453

RESULT 8
B98131
hypothetical protein AGR_L_30 [imported] - Agrobacterium tumefaciens (strain C58, Cereon
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98131
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B98131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-204 <KUR>
A;Cross-references: UNIPROT:Q8U6D2; GB:AE007870; PIDN:AAK88572.1; PID:g15158281; GSPDB:G
C;Genetics:
A;Gene: AGR_L_30
A;Map position: linear chromosome

Query Match 36.7%; Score 54; DB 2; Length 204;
Best Local Similarity 46.2%; Pred. No. 1.2;
Matches 12; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAMIPE 26
Db 50 SSRGNDLILPTSNKKWLRRRHAMSRE 75

RESULT 9
AG3156
conserved hypothetical protein Atu4875 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG3156
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyaivin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG3156
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-204 <KUR>

A;Cross-references: UNIPROT:Q8U6D2; GB:AE008689; PIDN:AAL45669.1; PID:g17743395; GSPDB: A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4875
A;Map position: linear chromosome

Query Match 36.7%; Score 54; DB 2; Length 204;
Best Local Similarity 46.2%; Pred. No. 1.2;
Matches 12; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAMIPE 26
Db 50 SSRGNDLILPTSNKKWLRRRHAMSRE 75

RESULT 10
S59786
hypothetical protein YDR320c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D9798.10
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S59786
R;Du, Z.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of S. cerevisiae cosmid 9798.
A;Reference number: S59418
A;Accession: S59786
A;Molecule type: DNA
A;Residues: 1-668 <DUZ>
A;Cross-references: UNIPROT:Q06677; EMBL:U32517; NID:g914989; PID:g914999; GSPDB:GN00000
A;Experimental source: strain S288C (AB972)
C;Genetics:
A;Gene: SGD:SWA2; MIPS:YDR320c
A;Cross-references: SGD:S0002728
A;Map position: 4R

Query Match 36.4%; Score 53.5; DB 2; Length 668;
Best Local Similarity 44.0%; Pred. No. 5.3;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Qy 3 SGLAL-LYPTNRNKNWDRMSAMIPE 26
Db 435 SSMALELPSSKAKWKIKISNDPE 459

RESULT 11
D84248
hypothetical protein Vng0920h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84248
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laeky, ; Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; I
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84248
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-688 <STO>
A;Cross-references: UNIPROT:Q9HR07; GB:AE004437; NID:g10580480; PIDN:AAG19352.1; GSPDB
C;Genetics:
A;Gene: VNG0920H

Query Match 36.1%; Score 53; DB 2; Length 688;
Best Local Similarity 43.5%; Pred. No. 6.5;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAM 23
Db 109 AAGNVALLYGVVRDAWDHRTAAV 131

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 22:34:20 ; Search time 39 Seconds
(without alignments)
69.079 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRNKWDNRMSAMIPED 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	130	88.4	515	2	E84577	probable cytokinin
2	108	73.5	524	2	T09937	cytokinin oxidase
3	80	54.4	504	2	T49185	cytokinin oxidase-
4	77	52.4	512	2	B96785	hypothetical prote
5	63	42.9	534	2	T01500	cytokinin oxidase
6	63	42.9	534	2	T51929	cytokinin oxidase
7	58	39.5	575	2	T00807	probable cytokinin
8	54	36.7	204	2	B98131	hypothetical prote
9	54	36.7	204	2	AG3156	conserved hypothet
10	53.5	36.4	668	2	S59786	hypothetical prote
11	53	36.1	688	2	D84248	hypothetical prote
12	51.5	35.0	356	2	AG3612	glycerol kinase (E
13	49.5	33.7	523	2	T04332	glutamate-cysteine
14	49	33.3	80	2	H69824	hypothetical prote
15	49	33.3	280	2	E82099	phosphatidate cyti
16	49	33.3	466	1	IQEBV	replication initia
17	48	32.7	240	2	S75162	hypothetical prote
18	48	32.7	246	2	F97076	hypothetical prote
19	48	32.7	326	1	JQ1443	glycoprotein VP7 p
20	48	32.7	1070	2	C75506	hypothetical prote
21	47.5	32.3	227	2	F90622	ATP synthase F0 ch
22	47	32.0	156	2	AB0079	hypothetical prote
23	47	32.0	784	2	T45697	hypothetical prote
24	47	32.0	1051	2	S59791	probable membrane
25	47	32.0	1324	2	T01508	mismatch repair en
26	46.5	31.6	224	2	F70798	hypothetical prote
27	46.5	31.6	255	2	A87619	hypothetical prote
28	46	31.3	338	2	S75196	hypothetical prote
29	46	31.3	494	2	H83351	conserved hypothet

30	46	31.3	890	2	T30103	hypothetical prote
31	45.5	31.0	227	2	T11027	H+-transporting tw
32	45.5	31.0	227	2	T11185	H+-transporting tw
33	45.5	31.0	227	2	T10991	H+-transporting tw
34	45.5	31.0	287	2	AG2414	hypothetical prote
35	45.5	31.0	568	2	T05218	hypothetical prote
36	45	30.6	350	2	D71348	flagellar filament
37	44.5	30.3	209	2	S31071	rpcF protein - Syn
38	44.5	30.3	499	2	AD3035	glycerol kinase gl
39	44.5	30.3	507	2	G98250	probable carbohydr
40	44.5	30.3	872	2	E71852	valine-tRNA ligase
41	44.5	30.3	874	2	A64664	valine-tRNA ligase
42	44.5	30.3	1075	2	AF2355	hypothetical prote
43	44	29.9	116	2	F82841	hypothetical prote
44	44	29.9	152	2	A41222	ubiquitin-protein
45	44	29.9	152	2	B41222	ubiquitin-protein

ALIGNMENTS

RESULT 1

E84577

probable cytokinin oxidase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 19-Apr-2002

C;Accession: E84577

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84577

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-515 <STO>

A;Cross-references: GB:AE002093; NID:g4191780; PIDN:AAD10149.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g19500

A;Map position: 2

C;Superfamily: poppy reticuline oxidase

Query Match 88.4%; Score 130; DB 2; Length 515;
Best Local Similarity 66.7%; Pred. No. 8.9e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 SASGLALLYPTNRN-----KWDNRMSAMIPED 28

Db 391 SASGLALLYPTNRNKYILLFIHYLQEPKWDNRMSAMIPED 432

RESULT 2

T09937

cytokinin oxidase homolog T16L4.250 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T09937

R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16897

A;Accession: T09937

A;Molecule type: DNA

A;Residues: 1-524 <BEV>

A;Cross-references: UNIPROT:Q9FUJ2; EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.250

A;Experimental source: cultivar Columbia; BAC clone T16L4

C;Genetics:

A;Gene: ATSP:T16L4.250

A;Map position: 4

A;Introns: 210/1; 252/3; 338/3; 428/2

Query Match 73.5%; Score 108; DB 2; Length 524;
Best Local Similarity 67.9%; Pred. No. 2e-08;

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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146464
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47086C.1.p
US-10-437-963-146464

Query Match 59.2%; Score 87; DB 16; Length 558;
Best Local Similarity 59.3%; Pred. No. 6.6e-05;
Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 ASGLALLYPTNRNKKWDNRMSAMIPED 28
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Db 440 AMGPVLIYPMNRNKKWDSNMSAVITDDD 466

RESULT 15

US-10-425-114-40061
; Sequence 40061, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40061
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700978152_FLI.p
US-10-425-114-40061

Query Match 57.8%; Score 85; DB 15; Length 292;
Best Local Similarity 57.7%; Pred. No. 6.7e-05;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 SGLALLYPTNRNKKWDNRMSAMIPED 28
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Db 172 SGPILLYPMNRNKKWDRSSVVTPEED 197

Search completed: February 22, 2005, 22:56:47
Job time : 131 secs

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; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39759
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700731265_FLI.pep
US-10-425-114-39759

Query Match          61.9%; Score 91; DB 15; Length 290;
Best Local Similarity 53.6%; Pred. No. 7.5e-06;
Matches 15; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 SASGLALLYPTNRNKWDNRMSAMIPEID 28
Db      170 TSNGPVLIIYPVNKSKWDNRRTSVVPIPED 197

RESULT 11
US-10-424-599-144567
; Sequence 144567, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 144567
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101557C.1.pep
US-10-424-599-144567

Query Match          61.9%; Score 91; DB 15; Length 324;
Best Local Similarity 53.6%; Pred. No. 8.5e-06;
Matches 15; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 SASGLALLYPTNRNKWDNRMSAMIPEID 28
Db      204 TSNGPVLIIYPVNKSKWDNRRTSVVPIPED 231

RESULT 12
US-10-425-114-42126
; Sequence 42126, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42126
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700985454_FLI.pep
US-10-425-114-42126

Query Match          61.9%; Score 91; DB 15; Length 324;
Best Local Similarity 53.6%; Pred. No. 8.5e-06;
Matches 15; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 SASGLALLYPTNRNKWDNRMSAMIPEID 28
Db      204 TSNGPVLIIYPVNKSKWDNRRTSVVPIPED 231

RESULT 13
US-10-437-963-148492
; Sequence 148492, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148492
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48918C.1.pep
US-10-437-963-148492

Query Match          59.9%; Score 88; DB 16; Length 525;
Best Local Similarity 61.5%; Pred. No. 4.3e-05;
Matches 16; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      1 SASGLALLYPTNRNKWDNRMSAMIPE 26
Db      404 SNGPILLIYPVNRTKWDNRRTSVVIPD 429

RESULT 14
US-10-437-963-146464
; Sequence 146464, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
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US-10-311-453-8
; Sequence 8, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-8

Query Match 73.5%; Score 108; DB 15; Length 524;
Best Local Similarity 67.9%; Pred. No. 3e-08;
Matches 19; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 SASGLALLYPTNRNKNWDRMSAMIPEID 28
|||:|||||:|||||:|:
Db 414 STSGVTLFYPTNRNKNWDRMSTMTPEID 441

RESULT 7
US-10-014-101-6
; Sequence 6, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-6

Query Match 65.3%; Score 96; DB 14; Length 523;
Best Local Similarity 69.2%; Pred. No. 2.4e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 SGLALLYPTNRNKNWDRMSAMIPEID 28
|||:|||||:|||||:|:
Db 411 SGPVLVYPMNRNKNWDRMSAAIPEED 436

RESULT 8
US-10-311-453-6

; Sequence 6, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-6

Query Match 65.3%; Score 96; DB 15; Length 523;
Best Local Similarity 69.2%; Pred. No. 2.4e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 SGLALLYPTNRNKNWDRMSAMIPEID 28
|||:|||||:|||||:|:
Db 411 SGPVLVYPMNRNKNWDRMSAAIPEED 436

RESULT 9
US-10-424-599-144566
; Sequence 144566, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 144566
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101556C.1.pep
US-10-424-599-144566

Query Match 61.9%; Score 91; DB 15; Length 290;
Best Local Similarity 53.6%; Pred. No. 7.5e-06;
Matches 15; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 SASGLALLYPTNRNKNWDRMSAMIPEID 28
:::|:|:|:|:|:|:|:|:|:
Db 170 TSNGPVLIVPNKSKWDNRTSVVIPEED 197

RESULT 10
US-10-425-114-39759
; Sequence 39759, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

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RESULT 2
US-10-311-453-32
; Sequence 32, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmlling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-32

Query Match      100.0%; Score 147; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.7e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 SASGLALLYPTNRNKKWDNRMSAMPEID 28
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      |||||||

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RESULT 3
 US-10-014-101-4
 ; Sequence 4, Application US/10014101
 ; Publication No. US20030074698A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmulling, Thomas
 ; APPLICANT: Werner, Tom B
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
 ; TITLE OF INVENTION: physiology
 ; FILE REFERENCE: 1195-2
 ; CURRENT APPLICATION NUMBER: US/10/014,101
 ; CURRENT FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833
 ; PRIOR FILING DATE: 2001-06-16
 ; PRIOR APPLICATION NUMBER: EP 00870132.8
 ; PRIOR FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: US 60/258,415
 ; PRIOR FILING DATE: 2000-12-27
 ; PRIOR APPLICATION NUMBER: EP 01870053.4
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 501
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 US-10-014-101-4

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Query Match      100.0%; Score 147; DB 14; Length 501;
Best Local Similarity 100.0%; Pred. No. 2.le-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASGLALLYPTNRNKWDNRMSAMPEID 28
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Db      391 SASGLALLYPTNRNKWDNRMSAMPEID 418

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RESULT 6

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RESULT 4
US-10-311-453-4
; Sequence 4, Application US/103111453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-4

Query Match      100.0%; Score 147; DB 15; Length 501;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 SASGLALYPTNRNKKWDNRMSAMPEID 28
Db      391 SASGLALYPTNRNKKWDNRMSAMPEID 418

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RESULT 5
 US-10-014-101-8.
 ; Sequence 8, Application US/10014101
 ; Publication No. US20030074698A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmulling, Thomas
 ; APPLICANT: werner, Tom s
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
 ; FILE REFERENCE: 1195-2
 ; CURRENT APPLICATION NUMBER: US/10/014,101
 ; CURRENT FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833
 ; PRIOR FILING DATE: 2001-06-16
 ; PRIOR APPLICATION NUMBER: EP 00870132.8
 ; PRIOR FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: US 60/258,415
 ; PRIOR FILING DATE: 2000-12-27
 ; PRIOR APPLICATION NUMBER: EP 01870053.4
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-014-101-8

RESULT 6

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRNKNWDRMSAMIPEID 28

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Total number of hits satisfying chosen parameters: 1380268

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	147	100.0	28	15	US-10-311-453-32
3	147	100.0	501	14	US-10-014-101-4
4	147	100.0	501	15	US-10-311-453-4
5	108	73.5	524	14	US-10-014-101-8
6	108	73.5	524	15	US-10-311-453-8
7	96	65.3	523	14	US-10-014-101-6
8	96	65.3	523	15	US-10-311-453-6
9	91	61.9	290	15	US-10-424-599-144566
10	91	61.9	290	15	US-10-425-114-39759
11	91	61.9	324	15	US-10-424-599-144567
12	91	61.9	324	15	US-10-425-114-42126
13	88	59.9	525	16	US-10-437-963-148492

14	87	59.2	558	16	US-10-437-963-146464	Sequence 146464,
15	85	57.8	292	15	US-10-425-114-40061	Sequence 40061, A
16	85	57.8	299	15	US-10-424-599-162425	Sequence 162425,
17	85	57.8	550	16	US-10-437-963-186310	Sequence 186310,
18	83	56.5	173	15	US-10-425-114-52875	Sequence 52875, A
19	83	56.5	521	16	US-10-437-963-173054	Sequence 173054,
20	82	55.8	143	15	US-10-424-599-205473	Sequence 205473,
21	81	55.1	534	16	US-10-437-963-140653	Sequence 140653,
22	80	54.4	504	14	US-10-014-101-12	Sequence 12, Appl
23	80	54.4	504	15	US-10-311-453-12	Sequence 12, Appl
24	77	52.4	536	14	US-10-014-101-10	Sequence 10, Appl
25	77	52.4	536	15	US-10-311-453-10	Sequence 10, Appl
26	77	52.4	539	14	US-10-014-101-35	Sequence 35, Appl
27	77	52.4	539	15	US-10-311-453-35	Sequence 35, Appl
28	75	51.0	214	15	US-10-424-599-200943	Sequence 200943,
29	75	51.0	527	16	US-10-437-963-136938	Sequence 136938,
30	74	50.3	532	16	US-10-437-963-183757	Sequence 183757,
31	68	46.3	517	16	US-10-437-963-177713	Sequence 177713,
32	66	44.9	392	15	US-10-425-114-39823	Sequence 39823, A
33	66	44.9	513	15	US-10-424-599-220961	Sequence 220961,
34	64	43.5	229	15	US-10-425-114-39997	Sequence 39997, A
35	64	43.5	230	15	US-10-424-599-255266	Sequence 255266,
36	63	42.9	611	9	US-09-829-549A-48	Sequence 48, Appl
37	59	40.1	164	16	US-10-437-963-173076	Sequence 173076,
38	58	39.5	99	15	US-10-424-599-204492	Sequence 204492,
39	58	39.5	99	15	US-10-425-114-56907	Sequence 56907, A
40	58	39.5	575	14	US-10-014-101-2	Sequence 2, Appli
41	58	39.5	575	15	US-10-311-453-2	Sequence 2, Appli
42	57	38.8	532	16	US-10-437-963-191047	Sequence 191047,
43	51	34.7	395	16	US-10-437-963-204083	Sequence 204083,
44	51	34.7	572	16	US-10-437-963-189286	Sequence 189286,
45	50	34.0	248	16	US-10-437-963-185716	Sequence 185716,

ALIGNMENTS

RESULT 1

US-10-014-101-32
; Sequence 32, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-32

Query Match 100.0%; Score 147; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.7e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAMIPEID 28

Db 1 SASGLALLYPTNRNKNWDRMSAMIPEID 28

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; LENGTH: 286
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9994

Query Match      30.6%; Score 45; DB 4; Length 286;
Best Local Similarity 36.4%; Pred. No. 40;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      4 GLALLYPTNRNKNWDRMSAMIP 25
      | | | | | : | | | : |
Db      225 GAALVYPGLGHRWVNRLLPLLP 246

RESULT 15
US-09-270-767-46433
; Sequence 46433, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46433
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46433

Query Match      30.6%; Score 45; DB 4; Length 314;
Best Local Similarity 45.5%; Pred. No. 45;
Matches 10; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      2 ASGLALLYPTNRNKNWDRMSAM 23
      | | | | | : | | | | |
Db      288 AFNLHLIYRANGNKWKARQYLM 309
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Db 427 ARLYNTNEANANARLSAMPLPV 448

RESULT 12

US-07-973-320-2
; Sequence 2, Application US/07973320
; Patent No. 5286486
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Fu, Jenny M.
; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,320
; FILING DATE: 19921106
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/788,638
; FILING DATE: 6-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA68.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1138 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: dakota
; INDIVIDUAL ISOLATE: HD511
; IMMEDIATE SOURCE:
; LIBRARY: Lamdagem (TM)-11 library of J.M. Fu
; CLONE: 511
US-07-973-320-2

Query Match 31.3%; Score 46; DB 1; Length 1138;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 LLYPTNRNKNWDRMS 21
||:|:|:|:|:|:
Db 91 LLWPHNKNIWDEFMT 105

RESULT 13

US-07-973-320-4
; Sequence 4, Application US/07973320
; Patent No. 5286486
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Fu, Jenny M.

; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,320
; FILING DATE: 19921106
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/788,638
; FILING DATE: 6-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA68.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1138 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: HD867
; IMMEDIATE SOURCE:
; LIBRARY: Lamdagem (TM)-11 library of J.M. Fu
; CLONE: 867
US-07-973-320-4

Query Match 31.3%; Score 46; DB 1; Length 1138;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 LLYPTNRNKNWDRMS 21
||:|:|:|:|:|:
Db 91 LLWPHNKNIWDEFMT 105

RESULT 14

US-09-902-540-9994
; Sequence 9994, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9994


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RESULT 7
US-09-911-882-14
; Sequence 14, Application US/09911882
; Patent No. 6465198
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062004
; CURRENT APPLICATION NUMBER: US/09/911,882
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-911-882-14
Query Match      32.0%; Score 47; DB 4; Length 1051;
Best Local Similarity 53.8%; Pred. No. 90;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      16 WDNRMSAMPEID 28
      ||: ||: ||: ||: ||
Db      796 WDDLQSSVPEVD 808

RESULT 8
US-09-911-888-14
; Sequence 14, Application US/09911888
; Patent No. 6514715
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062002
; CURRENT APPLICATION NUMBER: US/09/911,888
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-911-888-14
Query Match      32.0%; Score 47; DB 4; Length 1051;
Best Local Similarity 53.8%; Pred. No. 90;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      16 WDNRMSAMPEID 28
      ||: ||: ||: ||: ||
Db      796 WDDLQSSVPEVD 808

RESULT 9
US-09-270-767-60682
; Sequence 60682, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60682
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; LENGTH: 280
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60682
Query Match      31.3%; Score 46; DB 4; Length 280;
Best Local Similarity 43.8%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      10 PTNRNKWDNRMSAMIP 25
      ||||: ||: ||: ||: ||
Db      245 PTNRDLFDSAELVMVP 260

RESULT 10
US-09-248-796A-15064
; Sequence 15064, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15064
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15064
Query Match      31.3%; Score 46; DB 4; Length 466;
Best Local Similarity 32.1%; Pred. No. 50;
Matches 9; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY      1 SASGLALLYPTNRNKWDNRMSAMPEID 28
      ||||: ||: ||: ||: ||: ||
Db      407 SASAALLQALTKTQWLNRSLSILOQSV 434

RESULT 11
US-09-252-991A-25323
; Sequence 25323, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25323
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25323
Query Match      31.3%; Score 46; DB 4; Length 551;
Best Local Similarity 45.5%; Pred. No. 61;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      6 ALLYPTNRNKWDNRMSAMPEI 27
      ||||: ||: ||: ||: ||: ||
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Best Local Similarity 44.0%; Pred. No. 0.11;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 4 GLALLYPTNRNKNWDRMSAMPEID 28
Db 426 GPLIVYPLNKSMDGMSAATPSED 450

RESULT 3
US-08-728-603-19
; Sequence 19, Application US/08728603
; Patent No. 6093806
; GENERAL INFORMATION:
; APPLICANT: Cesarman, Ethel
; APPLICANT: Knowles, Daniel M.
; TITLE OF INVENTION: PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,603
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-728-603-19

Query Match 33.3%; Score 49; DB 3; Length 257;
Best Local Similarity 37.0%; Pred. No. 8.1;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 SASGLALLYPTNRNKNWDRMSAMPEI 27
Db 198 SAAGCALLVPANVIPQDTHSGGVVPQL 224

RESULT 4
US-09-543-681A-7393
; Sequence 7393, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 7393
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7393

Query Match 33.3%; Score 49; DB 4; Length 470;
Best Local Similarity 39.1%; Pred. No. 17;
Matches 9; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

Qy 10 PTN----RNKWDNRMSAMPEID 28
Db 108 PTNSQPVPRPSWDNQPSQLPELN 130

RESULT 5
US-08-965-762-14
; Sequence 14, Application US/08965762
; Patent No. 6280963
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 07334/062001
; CURRENT APPLICATION NUMBER: US/08/965,762
; CURRENT FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-08-965-762-14

Query Match 32.0%; Score 47; DB 3; Length 1051;
Best Local Similarity 53.8%; Pred. No. 90;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 16 WDNRMSAMPEID 28
Db 796 WDDLQSSVIPEVD 808

RESULT 6
US-09-911-927-14
; Sequence 14, Application US/09911927
; Patent No. 6461826
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062003
; CURRENT APPLICATION NUMBER: US/09/911,927
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-911-927-14

Query Match 32.0%; Score 47; DB 4; Length 1051;
Best Local Similarity 53.8%; Pred. No. 90;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 16 WDNRMSAMPEID 28
Db 796 WDDLQSSVIPEVD 808

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OM protein - protein search, using sw model

Run on: February 22, 2005, 22:35:25 ; Search time 42 Seconds
(without alignments)
49.766 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRKWKDNRMSAMPEID 28

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	63	42.9	534	3	US-09-124-541-1	Sequence 1, Appli
2	63	42.9	534	4	US-09-663-326-1	Sequence 1, Appli
3	49	33.3	257	3	US-08-728-603-19	Sequence 19, Appl
4	49	33.3	470	4	US-09-543-681A-7393	Sequence 7393, Ap
5	47	32.0	1051	3	US-08-965-762-14	Sequence 14, Appl
6	47	32.0	1051	4	US-09-911-927-14	Sequence 14, Appl
7	47	32.0	1051	4	US-09-911-882-14	Sequence 14, Appl
8	47	32.0	1051	4	US-09-911-888-14	Sequence 14, Appl
9	46	31.3	280	4	US-09-270-767-60682	Sequence 60682, A
10	46	31.3	466	4	US-09-248-796A-15064	Sequence 15064, A
11	46	31.3	551	4	US-09-252-991A-25323	Sequence 25323, A
12	46	31.3	1138	1	US-07-973-320-2	Sequence 2, Appli
13	46	31.3	1138	1	US-07-973-320-4	Sequence 4, Appli
14	45	30.6	286	4	US-09-902-540-9994	Sequence 9994, Ap
15	45	30.6	314	4	US-09-270-767-46433	Sequence 46433, A
16	45	30.6	938	4	US-09-602-787A-172	Sequence 172, App
17	44.5	30.3	795	4	US-09-248-796A-16677	Sequence 16677, A
18	44.5	30.3	872	1	US-08-451-715A-8	Sequence 8, Appli
19	44	29.9	130	4	US-09-621-976-4511	Sequence 4511, Ap
20	44	29.9	147	4	US-09-602-787A-252	Sequence 252, App
21	44	29.9	152	1	US-08-318-947A-6	Sequence 6, Appli
22	44	29.9	152	1	US-08-318-947A-7	Sequence 7, Appli
23	44	29.9	152	1	US-08-318-947A-8	Sequence 8, Appli
24	44	29.9	152	2	US-08-795-303-6	Sequence 6, Appli
25	44	29.9	152	2	US-08-795-303-7	Sequence 7, Appli
26	44	29.9	152	2	US-08-795-303-8	Sequence 8, Appli
27	44	29.9	152	2	US-08-247-904B-16	Sequence 16, Appli

28	44	29.9	152	3	US-08-767-942A-17	Sequence 17, Appl
29	44	29.9	152	4	US-09-538-092-1000	Sequence 1000, Ap
30	44	29.9	152	4	US-09-538-092-1155	Sequence 1155, Ap
31	44	29.9	257	4	US-09-949-016-8138	Sequence 8138, Ap
32	44	29.9	296	4	US-09-902-540-11571	Sequence 11571, A
33	44	29.9	383	4	US-09-107-532A-5105	Sequence 5105, Ap
34	44	29.9	571	2	US-08-796-414B-1	Sequence 1, Appli
35	44	29.9	571	4	US-09-543-681A-4700	Sequence 4700, Ap
36	44	29.9	619	4	US-09-252-991A-26352	Sequence 26352, A
37	43	29.3	152	4	US-09-216-430C-12	Sequence 12, Appl
38	43	29.3	152	4	US-09-216-430C-13	Sequence 13, Appl
39	43	29.3	165	4	US-09-252-991A-31564	Sequence 31564, A
40	43	29.3	264	4	US-09-270-767-42050	Sequence 42050, A
41	43	29.3	279	3	US-09-134-001C-4707	Sequence 4707, Ap
42	43	29.3	671	4	US-09-902-540-14154	Sequence 14154, A
43	43	29.3	2887	3	US-08-462-467B-2	Sequence 2, Appli
44	42.5	28.9	301	4	US-09-252-991A-21456	Sequence 21456, A
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ALIGNMENTS

RESULT 1
US-09-124-541-1
; Sequence 1, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Zea mays
US-09-124-541-1

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Best Local Similarity 44.0%; Pred. No. 0.11;
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; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Zea mays
US-09-663-326-1

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Query Match 42.9%; Score 63; DB 4; Length 534;

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PR 16-MAR-2001; 2001EP-00870053.
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PA (WERN/) WERNER T.
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PI Schmulling T, Werner T;
XX
DR WPI; 2002-130736/17.
DR N-PSDB; ABK28609.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 135-137; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. AAU81967-AAU81974 represent Arabidopsis thaliana cytokinin oxidase
CC amino acid sequences
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Query Match 73.5%; Score 108; DB 5; Length 524;
Best Local Similarity 67.9%; Pred. No. 1.1e-08;
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Search completed: February 22, 2005, 22:41:12
Job time : 168 secs

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XX AAG31316;

DT 17-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides
XX
SQ Sequence 515 AA;

Query Match      88.4%; Score 130; DB 5; Length 515;
Best Local Similarity 66.7%; Pred.No. 2.6e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

,QY 1 SASGLALLYPTNRN-----KWDNRMSAMIPEID 28
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RESULT 11
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XX
AC AAG31318;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37591.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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Query Match 88.4%; Score 130; DB 3; Length 515;
Best Local Similarity 66.7%; Pred. No. 2.6e-12;
Matches 28; Conservative 0; Mismatches 0; Indels

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Dd

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ID ABB91811 standard; protein; 515 AA.

AC ABB91811:

XX
DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 1022.

XX
KW Herbicidal; plant; agriculture; herbicide.

XX
OS *Arabidopsis thaliana*.

XX
PN WO200210210-A2.

XX
PD 07-FEB-2002.

XX
PF 28-AUG-2001; 2001WO-EP009892.

XX
PR 28-AUG-2001; 2001WO-EP009892.

XX
PA (FARB) BAYER AG.

XX
PI Tietjen K, Weidler M;

XX
DR WPI; 2002-269010/31.

xx Identifying plant target proteins for herbicidally active compounds,
 pt comprising aligning and comparing nucleic acid or amino acid sequences
 pt from plant with nucleic acid or amino acid sequences from non-plant
 pt organisms.

XX
PS Claim 5; SEQ ID NO 1022; 261pp + Sequence Listing; English.

XX
CC The invention relates to identifying target proteins (ABB90790-ABB94016)

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Query Match 88.4%; Score 130; DB 3; Length 509;
Best Local Similarity 66.7%; Pred. No. 2.5e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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RESULT 9
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ID AAG31940 standard; protein; 515 AA.

XX AAG31940;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 38444.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

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PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.

KW metal deficiency; nutrition; cytokinin oxidase; enzyme.

XX Arabidopsis thaliana.

PN WO2004038027-A1.

PD 06-MAY-2004.

XX 24-OCT-2003; 2003WO-EP012051.

XX 24-OCT-2002; 2002EP-00079481.

PA (CROP-) CROPDESIGN NV.

XX Van Camp W;

DR WPI; 2004-375913/35.

DR N-PSDB; ADO06498.

XX Method for bioremediation, useful for removing contaminants or metals, by decreasing cytokinin availability in plants, and cultivating plant on substrate comprising one or more contaminants.

PS Claim 8; Page 55-56; 6lpp; English.

XX The present invention relates to a method for bioremediation, which involves decreasing cytokinin availability in a plant relative to a corresponding wild type plant, and cultivating the plant on a substrate comprising one or more contaminants, or cultivating a plant having lowered availability of cytokinin relative to corresponding wild type plants, on a substrate, which is to be treated. The method is useful for bioremediation, for concentration of contaminants in a plant, where the plant has a higher concentration of contaminants compared to a corresponding wild type plant. The metal contaminants include aluminum, americium, antimony, arsenic, barium, beryllium, bismuth, cadmium, caesium, cerium, chromium, copper, gallium, germanium, gold, indium, iridium, iron, lead, manganese, mercury, molybdenum, neptunium, osmium, palladium, platinum, plutonium, radium, rhodium, rubidium, ruthenium, scandium, selenium, silver, strontium, technetium, tellurium, thallium, tin, tungsten, uranium, vanadium or yttrium, preferably cadmium. The plant obtained by the method is useful in bioremediation. Transgenic plants with a lower availability of cytokinin are useful in the manufacture of a medicament for treatment of disorders arising from metal deficiencies, and as a medicament for improving animal or human nutrition. The present sequence is a protein shown in the exemplification of the invention.

XX SQ Sequence 501 AA;

Query Match 100.0%; Score 147; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASGLALYPTNRNKWDNRMSAMIPED 28

Db 391 SASGLALYPTNRNKWDNRMSAMIPED 418

RESULT 7

AAG31942

ID AAG31942 standard; protein; 501 AA.

XX AAG31942;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38446.

DE Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 23-APR-1999; 99US-0130891P.
XX 28-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
XX 06-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 18-MAY-1999; 99US-0134768P.
XX 19-MAY-1999; 99US-0134941P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135353P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 16-JUN-1999; 99US-0139453P.
XX 17-JUN-1999; 99US-0139492P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
XX 18-JUN-1999; 99US-0139456P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
XX 18-JUN-1999; 99US-0139459P.
XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
XX 18-JUN-1999; 99US-0139462P.
XX 18-JUN-1999; 99US-0139463P.
XX 18-JUN-1999; 99US-0139750P.
XX 18-JUN-1999; 99US-0139763P.
XX 21-JUN-1999; 99US-0139817P.
XX 22-JUN-1999; 99US-0139899P.
XX 23-JUN-1999; 99US-0140353P.
XX 23-JUN-1999; 99US-0140354P.
XX 24-JUN-1999; 99US-0140695P.
XX 28-JUN-1999; 99US-0140823P.
XX 29-JUN-1999; 99US-0140991P.
XX 30-JUN-1999; 99US-0141287P.

CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. AAU81967-AAU81974 represent Arabidopsis thaliana cytokinin oxidase
CC amino acid sequences
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 147; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASGLALLYPTNRNKWDNRMSAMIPEID 28
|||
Db 1 SASGLALLYPTNRNKWDNRMSAMIPEID 28

RESULT 2
ABR63574
ID ABR63574 standard; peptide; 28 AA.

XX ABR63574;

AC ABR63574;

XX 18-SEP-2003 (first entry)

DE Arabidopsis cytokinin oxidase-like protein 2 fragment.

XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;

KW embryo size; cotyledon size; transgenic plant; herbicide.

XX Arabidopsis thaliana.

OS WO2003050287-A2.

PN 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.

PF 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

PI WPI; 2003-541577/51.

DR Stimulating root growth, enhancing lateral or adventitious root formation

XX or altering root geotropism comprises increasing plant cytokinin oxidase

CC levels or other protein or nucleic acid that reduces active cytokinins in

PT a plant.

XX Claim 3; Page 172; 177pp; English.

CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a protein shown in
CC the invention

XX Sequence 28 AA;
SQ Query Match 100.0%; Score 147; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASGLALLYPTNRNKWDNRMSAMIPEID 28
|||
Db 1 SASGLALLYPTNRNKWDNRMSAMIPEID 28

RESULT 3
AAU81968
ID AAU81968 standard; protein; 501 AA.

XX AAU81968;

AC 09-APR-2002 (first entry)

XX A. thaliana cytokinin oxidase AtCKX2.

KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp.

XX Arabidopsis thaliana.

OS WO200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

XX 27-DEC-2000; 2000US-0258415P.

XX 16-MAR-2001; 2001EP-00870053.

PA (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

PI WPI; 2002-130736/17.

DR N-PSDB; ABK28607.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase

CC activity and the protein useful for stimulating root growth, enhancing

CC the formation of lateral or adventitious roots, altering root geotropism.

XX Claim 12; Page 129-131; 154pp; English.

CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. AAU81967-AAU81974 represent Arabidopsis thaliana cytokinin oxidase
CC amino acid sequences

XX Sequence 501 AA;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 22:18:46 ; Search time 166 Seconds
(without alignments)
65.237 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRNKWDNRMSAMIPED 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	28	5 AAU81973	Aau81973 A. thalia
2	147	100.0	28	6 ABR63574	Abr63574 Arabidops
3	147	100.0	501	5 AAU81968	Aau81968 A. thalia
4	147	100.0	501	6 ABR63565	Abr63565 Arabidops
5	147	100.0	501	6 ABR63569	Abr63569 Arabidops
6	147	100.0	501	8 ADO06499	Ado06499 A thalian
7	130	88.4	501	3 AAG31942	Aag31942 Arabidops
8	130	88.4	509	3 AAG31941	Aag31941 Arabidops
9	130	88.4	515	3 AAG31940	Aag31940 Arabidops
10	130	88.4	515	5 ABB91811	Abb91811 Herbicida
11	108	73.5	395	3 AAG31318	Aag31318 Arabidops
12	108	73.5	400	3 AAG31317	Aag31317 Arabidops
13	108	73.5	524	3 AAG31316	Aag31316 Arabidops
14	108	73.5	524	5 ABB93161	Abb93161 Herbicida
15	108	73.5	524	5 AAU81970	Aau81970 A. thalia
16	108	73.5	524	6 ABR63567	Abr63567 Arabidops
17	108	73.5	524	6 ABR63571	Abr63571 Arabidops
18	96	65.3	523	5 ABB93847	Abb93847 Herbicida
19	96	65.3	523	5 AAU81969	Aau81969 A. thalia
20	96	65.3	523	6 ABR63566	Abr63566 Arabidops
21	96	65.3	523	6 ABR63570	Abr63570 Arabidops
22	87	59.2	563	8 ADP03326	Adp03326 Rice grai
23	87	59.2	565	8 ADP03323	Adp03323 Rice grai
24	80	54.4	504	5 ABB92780	Abb92780 Herbicida
25	80	54.4	504	5 AAU81972	Aau81972 A. thalia

26	80	54.4	504	6 ABR63573	Abr63573 Arabidops
27	77	52.4	536	5 ABB91608	Abb91608 Herbicida
28	77	52.4	536	5 AAU81971	Aau81971 A. thalia
29	77	52.4	536	6 ABR63572	Abr63572 Arabidops
30	77	52.4	539	5 AAU81974	Aau81974 A. thalia
31	77	52.4	539	6 ABR63575	Abr63575 Arabidops
32	63	42.9	534	2 AAW93007	Aaw93007 Z. mays c
33	63	42.9	534	6 ABR63563	Abr63563 Maize cyt
34	63	42.9	535	3 AAB30691	Aab30691 Amino aci
35	63	42.9	611	5 AAE13725	Aae13725 pJE-7 pla
36	58	39.5	575	5 ABB92071	Abb92071 Herbicida
37	58	39.5	575	5 AAU81967	Aau81967 A. thalia
38	58	39.5	575	6 ABR63568	Abr63568 Arabidops
39	58	39.5	575	6 ABR63564	Abr63564 Arabidops
40	58	39.5	575	8 ADO06497	Ado06497 A thalian
41	52	35.4	269	3 AAB53146	Aab53146 Macaca mu
42	50	34.0	1322	8 ADI42574	Adi42574 Plant tra
43	50	34.0	1322	8 ADO62380	Ado62380 Transcrip
44	49	33.3	257	2 AAW37977	Aaw37977 Kaposi's
45	49	33.3	280	6 ABU49494	Abu49494 Protein e

ALIGNMENTS

RESULT 1
AAU81973
ID AAU81973 standard; peptide; 28 AA.
XX

AC AAU81973;

DT 09-APR-2002 (first entry)

XX A. thaliana cytokinin oxidase AtCKX2, peptide.

KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy.

XX Arabidopsis thaliana.

XX WO200196580-A2.

XX 20-DEC-2001.

PF 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

PR 27-DEC-2000; 2000US-0258415P.

XX 16-MAR-2001; 2001EP-00870053.

PA (SCHM/) SCHMULLING T.

XX (WERN/) WERNER T.

PI Schmullling T, Werner T;

XX WPI; 2002-130736/17.

DR N-PSDB; ABK28630.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase

PT activity and the protein useful for stimulating root growth, enhancing

PT the formation of lateral or adventitious roots, altering root geotropism.

XX Claim 3; Page 150; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel

CC plant protein (II) having cytokinin oxidase activity. (I) is useful for

CC production of transgenic plants, plant cells or tissues; for production

CC of altered plants, plant cell or tissues; and for effecting the

CC expression of (II) where (I) is operably linked to one or more control

CC sequences. The methods further comprises regenerating a plant from the

CC plant cell. (I) and (II) are useful for stimulating root growth;

CC enhancing the formation of lateral or adventitious roots; altering root

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/221,017B
;; FILING DATE: 23-DEC-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PP1182
;; FILING DATE: 31-DEC-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PP1546
;; FILING DATE: 30-JAN-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PP2911
;; FILING DATE: 09-APR-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/AU98/01023
;; FILING DATE: 10-DEC-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Monroy, Gladys H
;; REGISTRATION NUMBER: 32,430
;; REFERENCE/DOCKET NUMBER: 27340-20021.00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 1014:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2601 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: UNKNOWN
;; ORIGINAL SOURCE:
;; ORGANISM: PORYPHYROMONAS GINGIVALIS
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1...2601
US-09-221-017B-1014

Alignment Scores:
Pred. No.: 272 Length: 2601
Score: 49.00 Matches: 8
Percent Similarity: 64.71% Conservative: 3
Best Local Similarity: 47.06% Mismatches: 6
Query Match: 33.33% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-32 (1-28) x US-09-221-017B-1014 (1-2601)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAsp 17
Db 2230 TCCACATACTCTATCGCTATCTTATTCTCTGCAACACAGAGAGAGTGGGAT 2180

RESULT 40
US-08-770-379-20/c
; Sequence 20, Application US/08770379
; Patent No. 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

;;
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/770,379
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 52342
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32207 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Alignment Scores:
Pred. No.: 7.29e+03 Length: 32207
Score: 49.00 Matches: 10
Percent Similarity: 55.56% Conservative: 5
Best Local Similarity: 37.04% Mismatches: 12
Query Match: 33.33% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-32 (1-28) x US-08-770-379-20 (1-32207)

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Db 17675 AGCGCTGCAGGCTGTGCGCTGTGGTTCTCTGCCAACGTCATCCGCAGGATACCCACTCG 17616
Qy 21 SerAlaMetIleProGluIle 27
Db 17615 GGTGGGGTAGTTCCTCAGCTG 17595

Search completed: February 18, 2005, 14:16:23
Job time : 557 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 12:07:27 ; Search time 289 Seconds
(without alignments)
572.643 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRKNKWDNRMSAMIPED 28

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10014101 @CGN 1 1 354 @runat_16022005_075936_8410
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Database : Published Applications_NA:*

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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	147	100.0	84	17	US-10-311-453-31	Sequence 31, Appl
3	147	100.0	1506	14	US-10-014-101-26	Sequence 26, Appl
4	147	100.0	1506	16	US-10-326-184-8	Sequence 8, Appli
5	147	100.0	1506	17	US-10-311-453-26	Sequence 26, Appl
6	108	73.5	1575	9	US-09-938-842A-2089	Sequence 2089, Ap
7	108	73.5	1575	11	US-09-938-842A-2089	Sequence 2089, Ap
8	108	73.5	1575	14	US-10-014-101-28	Sequence 28, Appl
9	108	73.5	1575	16	US-10-326-184-10	Sequence 10, Appl
10	108	73.5	1575	17	US-10-311-453-28	Sequence 28, Appl
11	108	73.5	1655	16	US-10-326-184-20	Sequence 20, Appl
12	96.5	65.6	2991	14	US-10-014-101-3	Sequence 3, Appli
13	96.5	65.6	2991	17	US-10-311-453-3	Sequence 3, Appli
14	96	65.3	1572	14	US-10-014-101-27	Sequence 27, Appl
15	96	65.3	1572	16	US-10-326-184-9	Sequence 9, Appli
16	96	65.3	1572	17	US-10-311-453-27	Sequence 27, Appl
17	91	61.9	1141	17	US-10-425-114-10886	Sequence 10886, A
18	91	61.9	1142	17	US-10-424-599-1725	Sequence 1725, Ap
19	91	61.9	1279	17	US-10-425-114-8021	Sequence 8021, Ap
20	91	61.9	1587	17	US-10-424-599-1724	Sequence 1724, Ap
21	88	59.9	2054	18	US-10-437-963-46009	Sequence 46009, A
22	87	59.2	1677	18	US-10-437-963-43981	Sequence 43981, A
23	86	58.5	1617	18	US-10-817-483-28	Sequence 28, Appl
24	85	57.8	1023	17	US-10-425-114-10804	Sequence 10804, A
25	85	57.8	1045	17	US-10-424-599-19583	Sequence 19583, A
26	85	57.8	1673	18	US-10-437-963-83827	Sequence 83827, A
27	83	56.5	1042	17	US-10-425-114-15562	Sequence 15562, A
28	83	56.5	1560	18	US-10-817-483-26	Sequence 26, Appl
29	83	56.5	1670	18	US-10-437-963-70571	Sequence 70571, A
30	83	56.5	1887	18	US-10-425-115-35578	Sequence 35578, A
31	83	56.5	2782	14	US-10-014-101-7	Sequence 7, Appli
32	83	56.5	2782	17	US-10-311-453-7	Sequence 7, Appli
33	82	55.8	816	17	US-10-424-599-62631	Sequence 62631, A
34	81	55.1	1605	18	US-10-437-963-38170	Sequence 38170, A
35	80	54.4	1515	14	US-10-014-101-30	Sequence 30, Appl
36	80	54.4	1515	17	US-10-311-453-30	Sequence 30, Appl
37	79	53.7	482	18	US-10-021-323-9662	Sequence 9662, Ap
38	79	53.7	484	18	US-10-021-323-10415	Sequence 10415, A
39	79	53.7	788	18	US-10-767-795-2077	Sequence 2077, Ap
40	77	52.4	1611	14	US-10-014-101-29	Sequence 29, Appl
41	77	52.4	1611	17	US-10-311-453-29	Sequence 29, Appl
42	77	52.4	1620	14	US-10-014-101-34	Sequence 34, Appl
43	77	52.4	1620	17	US-10-311-453-34	Sequence 34, Appl
44	77	52.4	1623	16	US-10-326-184-12	Sequence 12, Appl
45	76	51.7	675	17	US-10-425-114-32791	Sequence 32791, A

ALIGNMENTS

RESULT 1
US-10-014-101-31
; Sequence 31, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16


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; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-31

Alignment Scores:
Pred. No.:          3.09e-17          Length:          84
Score:              147.00           Matches:         28
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:        100.00%           Indels:         0
DB:                 14                Gaps:          0

US-10-014-101B-32 (1-28) x US-10-014-101-31 (1-84)

QY      1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
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Db      1 TCAGCTTCGGGACTCGCTCTTCTCTATCCAAACCGGAATAAATGGGACAATCGTATG 60
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QY      21 SerAlaMetIleProGluIleAsp 28
      |||||||
Db      61 TCGGCGATGATACCAAGATCGAT 84
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RESULT 2
US-10-311-453-31
; Sequence 31, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-31
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Alignment Scores:
Pred. No.:          3.09e-17          Length:          84
Score:              147.00           Matches:         28
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:        100.00%           Indels:         0
DB:                 17                Gaps:          0

US-10-014-101B-32 (1-28) x US-10-311-453-31 (1-84)

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      |||||||
Db      1 TCAGCTTCGGGACTCGCTCTTCTCTATCCAAACCGGAATAAATGGGACAATCGTATG 60
      |||||||

QY      21 SerAlaMetIleProGluIleAsp 28
      |||||||
Db      61 TCGGCGATGATACCAAGATCGAT 84
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RESULT 3
US-10-014-101-26
; Sequence, 26, Application US/10014101
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; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-26
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Alignment Scores:
Pred. No.:          1.2e-15          Length:          1506
Score:              147.00           Matches:         28
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:        100.00%           Indels:         0
DB:                 14                Gaps:          0
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QY      21 SerAlaMetIleProGluIleAsp 28
      |||||||
Db      1231 TCGGCGATGATACCAAGATCGAT 1254
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RESULT 4
US-10-326-184-8
; Sequence 8, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C1
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-8
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Score:              147.00           Matches:         28
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:        100.00%           Indels:         0
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US-10-014-101B-32 (1-28) x US-10-326-184-8 (1-1506)


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; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-28

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Pred. No.: 1.07e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-014-101-28 (1-1575)

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QY 21 SerAlaMetIleProGluIleAsp 28
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RESULT 9
US-10-326-184-10
; Sequence 10, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-10

Alignment Scores:
Pred. No.: 1.07e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-326-184-10 (1-1575)

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QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTTCTATCCACAAACCGAAACAAATGGAACACCGCATG 1299
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 10
US-10-311-453-28
; Sequence 28, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-28

Alignment Scores:
Pred. No.: 1.07e-08 Length: 1575
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 67.86% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-311-453-28 (1-1575)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 1240 TCAACTTCTGGTGTACTCTCTTCTATCCACAAACCGAAACAAATGGAACACCGCATG 1299
QY 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 11
US-10-326-184-20
; Sequence 20, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-20

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Alignment Scores:
Pred. No.: 1.14e-08 Length: 1655
Score: 108.00 Matches: 19
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 73.47% Mismatches: 6
Query Match: 73.47% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-326-184-20 (1-1655)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAsnArgMet 20
Db 1240 TCAACTTCTGCTGTTACTCTCTCTATCCCAACCGAACAATGGAACACCGCATG 1299

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 1300 TCAACGATGACACCGGACGAAGAT 1323

RESULT 12
US-10-014-101-3
; Sequence 3, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-10-014-101-3
Alignment Scores:
Pred. No.: 2.67e-06 Length: 2991
Score: 96.50 Matches: 27
Percent Similarity: 48.21% Conservative: 0
Best Local Similarity: 48.21% Mismatches: 1
Query Match: 65.65% Indels: 29
DB: 14 Gaps: 1

US-10-014-101-3
Alignment Scores:
Pred. No.: 2.67e-06 Length: 2991
Score: 96.50 Matches: 27
Percent Similarity: 48.21% Conservative: 0
Best Local Similarity: 48.21% Mismatches: 1
Query Match: 65.65% Indels: 29
DB: 14 Gaps: 1

US-10-014-101B-32 (1-28) x US-10-014-101-3 (1-2991)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2573 TCAGCTTCGGGACTCGCTCTCTCTATCCCAACCGAATAA-GTACATACTTCTCTT 2631

Qy 15 ----- 15
Db 2632 CATTCAATTTATCTTCAAGAACCAAGTAAATAATTTCTATGAAGTATTGCTGTT 2691

Qy 16 -----TrpAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2692 ATTGTTAGATGGACAATCGTATGTCGGCGATGATACCAGAGATCGAT 2739

RESULT 13
US-10-311-453-3
; Sequence 3, Application US/10311453
; Publication No. US20040031073A1

GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-10-311-453-3
Alignment Scores:
Pred. No.: 2.67e-06 Length: 2991
Score: 96.50 Matches: 27
Percent Similarity: 48.21% Conservative: 0
Best Local Similarity: 48.21% Mismatches: 1
Query Match: 65.65% Indels: 29
DB: 17 Gaps: 1

US-10-014-101B-32 (1-28) x US-10-311-453-3 (1-2991)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2573 TCAGCTTCGGGACTCGCTCTCTCTATCCCAACCGAATAA-GTACATACTTCTCTT 2631

Qy 15 ----- 15
Db 2632 CATTCAATTTATCTTCAAGAACCAAGTAAATAATTTCTATGAAGTATTGCTGTT 2691

Qy 16 -----TrpAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2692 ATTGTTAGATGGACAATCGTATGTCGGCGATGATACCAGAGATCGAT 2739

RESULT 14
US-10-014-101-27
; Sequence 27, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-10-014-101-27
Alignment Scores:
Pred. No.: 2.67e-06 Length: 1572
Score: 96.50 Matches: 27
Percent Similarity: 48.21% Conservative: 0
Best Local Similarity: 48.21% Mismatches: 1
Query Match: 65.65% Indels: 29
DB: 14 Gaps: 1

Pred. No.: 1.45e-06 Length: 1572
Score: 96.00 Matches: 18
Percent Similarity: 80.77% Conservative: 3
Best Local Similarity: 69.23% Mismatches: 5
Query Match: 65.31% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-014-101-27 (1-1572)

QY 3 SerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1231 AGCGGTCTGTTCTTTATCCTATGAATCGCAACAAGTGAATGATCGGATGCTGCGC 1290

QY 23 MetIleProGluIleAsp 28
Db 1291 GCTATACCCGAGGAAGAT 1308

RESULT 15
US-10-326-184-9
; Sequence 9, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-9

Alignment Scores:
Pred. No.: 1.45e-06 Length: 1572
Score: 96.00 Matches: 18
Percent Similarity: 80.77% Conservative: 3
Best Local Similarity: 69.23% Mismatches: 5
Query Match: 65.31% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-326-184-9 (1-1572)

QY 3 SerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1231 AGCGGTCTGTTCTTTATCCTATGAATCGCAACAAGTGAATGATCGGATGCTGCGC 1290

QY 23 MetIleProGluIleAsp 28
Db 1291 GCTATACCCGAGGAAGAT 1308

RESULT 16
US-10-311-453-27
; Sequence 27, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4

; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-27

Alignment Scores:
Pred. No.: 1.45e-06 Length: 1572
Score: 96.00 Matches: 18
Percent Similarity: 80.77% Conservative: 3
Best Local Similarity: 69.23% Mismatches: 5
Query Match: 65.31% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-311-453-27 (1-1572)

QY 3 SerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 1231 AGCGGTCTGTTCTTTATCCTATGAATCGCAACAAGTGAATGATCGGATGCTGCGC 1290

QY 23 MetIleProGluIleAsp 28
Db 1291 GCTATACCCGAGGAAGAT 1308

RESULT 17
US-10-425-114-10886
; Sequence 10886, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10886
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700985454_FLI
US-10-425-114-10886

Alignment Scores:
Pred. No.: 7.45e-06 Length: 1141
Score: 91.00 Matches: 15
Percent Similarity: 78.57% Conservative: 7
Best Local Similarity: 53.57% Mismatches: 6
Query Match: 61.90% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-425-114-10886 (1-1141)

QY 1 SerAlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 610 ACTAGCAACGGCCCCGTCCTTATCTACCCAGTAAACAATCAAGTGGGACACAGAACT 669

QY 21 SerAlaMetIleProGluIleAsp 28
Db 670 TCTGTGTGATTCAGAGGAGAT 693

RESULT 18
US-10-424-599-1725
; Sequence 1725, Application US/10424599

```

; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1725
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101557C.1
US-10-424-599-1725

Alignment Scores:
Pred. No.: 7.46e-06 Length: 1142
Score: 91.00 Matches: 15
Percent Similarity: 78.57% Conservative: 7
Best Local Similarity: 53.57% Mismatches: 6
Query Match: 61.90% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-424-599-1725 (1-1142)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 611 ACTAGCAACGGCCCGTCCTTATCTACCCAGTAAACAATCAAAATGGGACACAGAACT 670

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 671 TCTGTTGTGATTCCAGAGGAAGAT 694

RESULT 19
US-10-425-114-8021
; Sequence 8021, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8021
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700731265_FLI
US-10-425-114-8021

Alignment Scores:
Pred. No.: 8.61e-06 Length: 1279
Score: 91.00 Matches: 15
Percent Similarity: 78.57% Conservative: 7
Best Local Similarity: 53.57% Mismatches: 6
Query Match: 61.90% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-425-114-8021 (1-1279)

```

```

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 689 ACACGCAACGGCCCTGTCTTATCTACCCAGTAAATAATCAAAATGGGACACAGAACT 748

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 749 TCTGTTGTGATTCCAGAGGAAGAT 772

RESULT 20
US-10-424-599-1724
; Sequence 1724, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1724
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1587)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101556C.1
US-10-424-599-1724

Alignment Scores:
Pred. No.: 1.13e-05 Length: 1587
Score: 91.00 Matches: 15
Percent Similarity: 78.57% Conservative: 7
Best Local Similarity: 53.57% Mismatches: 6
Query Match: 61.90% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-424-599-1724 (1-1587)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 726 ACACGCAACGGCCCTGTCTTATCTACCCAGTAAATAATCAAAATGGGACACAGAACT 785

Qy 21 SerAlaMetIleProGluIleAsp 28
Db 786 TCTGTTGTGATTCCAGAGGAAGAT 809

RESULT 21
US-10-437-963-46009
; Sequence 46009, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 46009

```



```
RESULT 28
US-10-817-483-26
; Sequence 26, Application US/10817483
; Publication No. US20040237147A1
; GENERAL INFORMATION:
; APPLICANT: Habben, Jeffrey E.
; APPLICANT: Zinselmeier, Christopher
; APPLICANT: Tomes, Dwight
; APPLICANT: Abbott, Shane
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Niu, Xiaomu
; TITLE OF INVENTION: Modulation of Cytokinin Activity in
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 0803R
; CURRENT APPLICATION NUMBER: US/10/817,483
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/460,718
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 09/545,334
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1560)
US-10-817-483-26
```

```
Alignment Scores:
Pred. No.: 0.000292 Length: 1560
Score: 83.00 Matches: 14
Percent Similarity: 76.92% Conservative: 6
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 56.46% Indels: 0
DB: 18 Gaps: 0
```

US-10-014-101B-32 (1-28) x US-10-817-483-26 (1-1560)

```
Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
||| ::::| ||||| ||||| ||||| ||||| ||||| ||||| ::::|
Db 1192 AGCAACAATGGTCCCTATATTGCTTTATCCAGTGAACAAATCAAAGTGGGACAAACG 1251
```

```
Qy 21 SerAlaMetIleProGlu 26
||| ::::| ||||| ::::|
Db 1252 TCAGTGGTCATACCAGAT 1269
```

```
RESULT 29
US-10-437-963-70571
; Sequence 70571, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 70571
; LENGTH: 1670
```

```
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7112C.1
US-10-437-963-70571

Alignment Scores:
Pred. No.: 0.000318 Length: 1670
Score: 83.00 Matches: 14
Percent Similarity: 76.92% Conservative: 6
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 56.46% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-437-963-70571 (1-1670)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
||| ::::| ||||| ||||| ||||| ||||| ||||| ::::|
Db 1305 AGTAACAATGGTCCCATATTACTCTATCCAGTGAACAAATCCAGATGGGACACAGAAC 1364

Qy 21 SerAlaMetIleProGlu 26
||| ::::| ||||| ::::|
Db 1365 TCAGTAGTCATACCAGAT 1382
```

RESULT 30

```
US-10-425-115-35578
; Sequence 35578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 35578
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_132445C.1
US-10-425-115-35578
```

```
Alignment Scores:
Pred. No.: 0.000372 Length: 1887
Score: 83.00 Matches: 14
Percent Similarity: 76.92% Conservative: 6
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 56.46% Indels: 0
DB: 18 Gaps: 0
```

US-10-014-101B-32 (1-28) x US-10-425-115-35578 (1-1887)

```
Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
||| ::::| ||||| ||||| ||||| ||||| ||||| ::::|
Db 941 AGCAACAATGGTCCCTATATTGCTTTATCCAGTGAACAAATCAAAGTGGGACAAACG 1000

Qy 21 SerAlaMetIleProGlu 26
||| ::::| ||||| ::::|
Db 1001 TCAGTGGTCATACCAGAT 1018
```

RESULT 31

```
US-10-014-101-7
; Sequence 7, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
```

; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-7

Alignment Scores:
Pred. No.: 0.000608 Length: 2782
Score: 83.00 Matches: 19
Percent Similarity: 37.93% Conservative: 3
Best Local Similarity: 32.76% Mismatches: 6
Query Match: 56.46% Indels: 30
DB: 14 Gaps: 1

US-10-014-101B-32 (1-28) x US-10-014-101-7 (1-2782)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2357 TCAACTTCTGGTGTTACTCTCTCTATCCCAAAACCGAACAAGTAAATATTTACTTTT 2416
Qy 15 ----- 15
Db 2417 TGATTTGTTTTATTGAAAGTATATCCCAATAATGTATGTTAAATGTTAAACAAGAATT 2476
Qy 16 -----TipAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2477 TATTTTATTAATAGATGGAACAACCGCATGTCAACGATGACACCGGACGAAGAT 2530

RESULT 32
US-10-311-453-7
; Sequence 7, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-7

Alignment Scores:
Pred. No.: 0.000608 Length: 2782
Score: 83.00 Matches: 19
Percent Similarity: 37.93% Conservative: 3
Best Local Similarity: 32.76% Mismatches: 6

Query Match: 56.46% Indels: 30
DB: 17 Gaps: 1
US-10-014-101B-32 (1-28) x US-10-311-453-7 (1-2782)
Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 2357 TCAACTTCTGGTGTTACTCTCTCTATCCCAAAACCGAACAAGTAAATATTTACTTTT 2416
Qy 15 ----- 15
Db 2417 TGATTTGTTTTATTGAAAGTATATCCCAATAATGTATGTTAAATGTTAAACAAGAATT 2476
Qy 16 -----TipAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 2477 TATTTTATTAATAGATGGAACAACCGCATGTCAACGATGACACCGGACGAAGAT 2530

RESULT 33
US-10-424-599-62631
; Sequence 62631, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 62631
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(816)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27570C.1
US-10-424-599-62631

Alignment Scores:
Pred. No.: 0.000193 Length: 816
Score: 82.00 Matches: 15
Percent Similarity: 78.26% Conservative: 3
Best Local Similarity: 65.22% Mismatches: 5
Query Match: 55.78% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-424-599-62631 (1-816)

Qy 4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTipAspAsnArgMetSerAlaMet 23
Db 90 GGACCAGTCTTGGTTTATCCCATGAATAGAAACAAGTGGTACGATAGGATGTCAGCATCT 149
Qy 24 IleProGlu 26
Db 150 ATACCAGAC 158

RESULT 34
US-10-437-963-38170
; Sequence 38170, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

OTHER INFORMATION: Clone ID: LIB3828-026-Q6-K6-E7
US-10-021-323-9662

Alignment Scores:
Pred. No.: 0.000338 Length: 482
Score: 79.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 53.74% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-021-323-9662 (1-482)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22

Db 107 AGTGGCCCAATTCTCATCTATCCAAATGAACAAGAACAAATGGGACCATAGGAGCTCCGTG 166

QY 23 MetIleProGlu 26

Db 167 GTGACACCGGAT 178

RESULT 38

US-10-021-323-10415/c

Sequence 10415, Application US/10021323

Publication No. US20040123340A1

GENERAL INFORMATION:

APPLICANT: Deikman, Jill

APPLICANT: Feng, Paul C.C.

APPLICANT: Fincher, Karen L.

APPLICANT: Ziegler, Todd E.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(52274)B

CURRENT APPLICATION NUMBER: US/10/021,323

CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 10415

LENGTH: 484

TYPE: DNA

ORGANISM: Gossypium hirsutum

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(484)

OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: LIB3828-026-Q6-N6-E7

US-10-021-323-10415

Alignment Scores:
Pred. No.: 0.00034 Length: 484
Score: 79.00 Matches: 13
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 54.17% Mismatches: 6
Query Match: 53.74% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-021-323-10415 (1-484)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22

Db 376 AGTGGCCCAATTCTCATCTATCCAAATGAACAAGAACAAATGGGACCATAGGAGCTCCGTG 317

QY 23 MetIleProGlu 26

Db 316 GTGACACCGGAT 305

RESULT 39

US-10-767-795-2077

Sequence 2077, Application US/10767795

Publication No. US20040181830A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 2077
LENGTH: 788
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:

OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C36643_1

US-10-767-795-2077

Alignment Scores:

Pred. No.: 0.000631 Length: 788

Score: 79.00 Matches: 13

Percent Similarity: 75.00% Conservative: 5

Best Local Similarity: 54.17% Mismatches: 6

Query Match: 53.74% Indels: 0

DB: 18 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-767-795-2077 (1-788)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22

Db 412 AGTGGCCCAATTCTCATCTATCCAAATGAACAAGAACAAATGGGACCATAGGAGCTCCGTG 471

QY 23 MetIleProGlu 26

Db 472 GTGACACCGGAT 483

RESULT 40

US-10-014-101-29

Sequence 29, Application US/10014101

Publication No. US20030074698A1

GENERAL INFORMATION:

APPLICANT: Schmulling, Thomas

APPLICANT: Werner, Tom S

TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and

TITLE OF INVENTION: physiology

FILE REFERENCE: 1195-2

CURRENT APPLICATION NUMBER: US/10/014,101

CURRENT FILING DATE: 2001-12-10

PRIOR APPLICATION NUMBER: PCT/EP01/06833

PRIOR FILING DATE: 2001-06-16

PRIOR APPLICATION NUMBER: EP 00870132.8

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/258,415

PRIOR FILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: EP 01870053.4

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 29

LENGTH: 1611

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-10-014-101-29

Alignment Scores:

Pred. No.: 0.00354 Length: 1611

Score: 77.00 Matches: 13

Percent Similarity: 75.00% Conservative: 5

Best Local Similarity: 54.17% Mismatches: 6

Query Match: 52.38% Indels: 0

DB: 14 Gaps: 0

US-10-014-101B-32 (1-28) x US-10-014-101-29 (1-1611)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22


```
Db      1213 AGTGGCCCTATTCTTATCTACCCCATGAACAAGACAAATGGGACGAGAGGAGCTCAGCC 1272
Qy      23 MetIleProGlu 26
Db      1273 GTGACGCCGGGAT 1284
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Search completed: February 18, 2005, 14:57:53
Job time : 295 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 09:14:12 ; Search time 7200 Seconds
(without alignments)
148.028 Million cell updates/sec

Title: US-10-014-101B-32
Perfect score: 147
Sequence: 1 SASGLALLYPTNRKNKWDNRMSAMPEID 28

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10014101/runat 16022005 075934 8314/app query.fasta.1.199
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -ENDS=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101 @CGN 1 1 2607 @runat 16022005 075934 8314 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_htc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	102	69.4	418	5	BP576449
C 2	100	68.0	593	7	CO979507
3	96	65.3	1594	3	CNS0A1GX
4	93	63.3	806	7	CF393540
5	92	62.6	539	4	BM138354
6	91	61.9	697	7	CF398227
C 7	88	59.9	401	1	AV810994
8	88	59.9	505	4	BI927011
C 9	88	59.9	642	4	BI926735

C 10	88	59.9	757	7	CO119329	CO119329 GR_Eb022
C 11	88	59.9	795	7	CO117913	CO117913 GR_Eb01P
12	88	59.9	807	6	CA766552	CA766552 AF53-Rpf
13	88	59.9	824	7	CO121610	CO121610 GR_Eb02N
14	88	59.9	1578	9	CL960490	CL960490 OsIFCC004
15	87	59.2	772	6	CB620527	CB620527 OSIIEa05N
16	87	59.2	863	7	CO435706	CO435706 OsMR772 5
17	87	59.2	1671	9	CL957466	CL957466 OsIFCC000
C 18	86.5	58.8	436	1	AU227876	AU227876 AU227876
19	86	58.5	438	4	BG518327	BG518327 947066A06
20	86	58.5	642	4	BI203744	BI203744 EST521784
21	86	58.5	715	4	BI204708	BI204708 EST522748
C 22	86	58.5	826	8	BZ644495	BZ644495 OGCCW96TM
C 23	86	58.5	906	9	CG289642	CG289642 OGWFN30TH
C 24	86	58.5	963	9	CG351153	CG351153 OG2BM20TV
25	85	57.8	584	6	CB913923	CB913923 VVD172F06
C 26	85	57.8	741	7	CF210007	CF210007 CAB20005
C 27	85	57.8	773	4	BI970438	BI970438 GM830010B
28	85	57.8	809	7	CF209921	CF209921 CAB20005
29	85	57.8	1587	9	CL964867	CL964867 OsIFCC011
C 30	84	57.1	757	7	CO174423	CO174423 NDL1_43_H
C 31	84	57.1	812	7	CO174338	CO174338 NDL1_43_H
32	83	56.5	481	1	AV536711	AV536711 AV536711
33	83	56.5	1566	9	CL947867	CL947867 OsIFSB001
34	82	55.8	575	2	BF520835	BF520835 EST458308
C 35	82	55.8	610	9	CC694028	CC694028 OGWEK48TH
C 36	82	55.8	636	6	CA918993	CA918993 EST636711
37	82	55.8	753	9	CC693605	CC693605 OGULX22TH
38	82	55.8	788	6	CF068302	CF068302 EST669023
C 39	82	55.8	831	7	CO483046	CO483046 GQ0198.TB
C 40	82	55.8	856	7	CO485966	CO485966 GQ02013.T
C 41	82	55.8	876	9	CG445712	CG445712 OGVHS26TV
42	82	55.8	969	9	CG289653	CG289653 OGWFN30TV
43	81	55.1	468	1	AI774379	AI774379 EST255479
C 44	80	54.4	589	7	CO490541	CO490541 GQ027M02
45	80	54.4	831	7	CN201821	CN201821 Tor1899 G

ALIGNMENTS

RESULT 1
BP576449/c

LOCUS
BP576449

DEFINITION
BP576449 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-92-C01 3',
mRNA sequence.

ACCESSION
BP576449

VERSION
BP576449.1 GI:48992215

KEYWORDS
EST.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana

REFERENCE
1 (bases 1 to 418)

AUTHORS
Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.

TITLE
Functional annotation of a full-length Arabidopsis cDNA collection

JOURNAL
Science 296 (5565), 141-145 (2002)

MEDLINE
21932900

PUBMED
11910074

COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekic@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
Location/Qualifiers
1. .418

source

REFERENCE 1 (bases 1 to 539)
AUTHORS Anderson,O.D., Chao,S., Han,P.S., Heinen,S., Hsia,C.C., Kang,Y., Kruger,W.M., Lazo,G.R., Miller,S., Muehlbauer,G.J., Miller,R., Pritsch,C., Rausch,C.J., Seaton,C.L., Tong,J.C., Vance,C. and Wilson,C.F.
TITLE The structure and function of the expressed portion of the wheat genomes - Fusarium graminearum infected spike cDNA library
JOURNAL Unpublished (2001)
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST could be of wheat or fungal origin.
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1..539
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/clone="WHE0491_F05_K09"
/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/clone_lib="Wheat Fusarium graminearum infected spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Spikes were sprayed at anthesis with Fusarium graminearum. Total RNA, and poly(A) RNA were prepared and pooled from infected spike at 0, 6, 12, 24, 36 and 48 hours after inoculation, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in G. Muehlbauer lab at the University of Minnesota (Kruger, W.M., Muehlbauer, G.J., Pritsch, C., Vance, C.). The cDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
ORIGIN
Alignment Scores:
Pred. No.: 0.000222 Length: 539
Score: 92.00 Matches: 17
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 65.38% Mismatches: 6
Query Match: 62.59% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-32 (1-28) x BM138354 (1-539)
Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 237 AGCAACAATGGCCCCATCCTCCTCTACCCAGTGAACAGATCAAAGTGGACACAGGACG 296
Qy 21 SerAlaMetIleProGlu 26
Db 297 TCAGTGGTGATACCGGAG 314
RESULT 6
CF398227
LOCUS CF398227 697 bp mRNA linear EST 29-AUG-2003
DEFINITION RTDS3_24_F01.b1_A022 Drought-stressed loblolly pine roots DS3 Pinus taeda cDNA clone RTDS3_24_F01_A022 3', mRNA sequence.
ACCESSION CF398227
VERSION CF398227.1 GI:34356644
KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 697)
AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.
TITLE An EST database from drought-stressed loblolly pine (Pinus taeda) roots
JOURNAL Unpublished (2003)
COMMENT Other ESTs: RTDS3_24_F01.g1_A022
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAACGACGCGCCAGT)
POLYA=Yes.
FEATURES Location/Qualifiers
source 1..697
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTDS3_24_F01_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Drought-stressed loblolly pine roots DS3"
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from drought-stressed loblolly pine (Pinus taeda) roots. Water was withheld from ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
ORIGIN
Alignment Scores:
Pred. No.: 0.000442 Length: 697
Score: 91.00 Matches: 16
Percent Similarity: 76.00% Conservative: 3
Best Local Similarity: 64.00% Mismatches: 6
Query Match: 61.90% Indels: 0
DB: 7 Gaps: 0
US-10-014-101B-32 (1-28) x CF398227 (1-697)
Qy 4 GlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
Db 203 GGGCGGTTCCTTATCTACCTGTGAACCGCAATAAGTGGGATAGCAGATGTCAGCGGTG 262
Qy 24 IleProGluIleAsp 28
Db 263 ACTCCTAATGAGGAC 277
RESULT 7
AV810994/c
LOCUS AV810994 401 bp mRNA linear EST 29-MAR-2002
DEFINITION AV810994 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-66-D02 3', mRNA sequence.
ACCESSION AV810994
VERSION AV810994.1 GI:19844979
KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 401)
REFERENCE Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
A large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
FEATURES Location/Qualifiers
source 1..401
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL09-66-D02"
/dev stage="plants at various developmental stages from germination to mature seeds"
/lab host="DH10B"
/clone_lib="RAFL9"
/note="Site_1: BamHI; Site_2: Sali; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
ORIGIN
Alignment Scores:
Pred. No.: 0.000685 Length: 401
Score: 88.00 Matches: 15
Percent Similarity: 75.00% Conservative: 6
Best Local Similarity: 53.57% Mismatches: 7
Query Match: 59.86% Indels: 0
DB: 1 Gaps: 0
US-10-014-101B-32 (1-28) x AV810994 (1-401)
Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 360 TCAACTTCGTGTACTCTCTTTATCCACCAACCGAACCATGAACCCCAT 301
Qy 21 SerAlaMetIleProGluIleAsp 28
Db 300 TCAACGATGACACCCGACGAAGAT 277
RESULT 8
BI927011
LOCUS BI927011 505 bp mRNA linear EST 18-OCT-2001
DEFINITION EST546900 tomato flower, buds 0-3 mm Lycopersicon esculentum cDNA clone CTOA31010 5' end, mRNA sequence.
ACCESSION BI927011
VERSION BI927011.1 GI:16236104
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 505)
REFERENCE

AUTHORS van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, 0-3 mm buds (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics Institute
Seq primer: T3.
FEATURES Location/Qualifiers
source 1..505
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTOA31010"
/tissue_type="flower"
/dev_stage="0-3mm buds"
/clone_lib="tomato flower, buds 0-3 mm"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
ORIGIN
Alignment Scores:
Pred. No.: 0.000909 Length: 505
Score: 88.00 Matches: 15
Percent Similarity: 87.50% Conservative: 6
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 59.86% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-32 (1-28) x BI927011 (1-505)
Qy 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 81 AATGGACCCATACCTTGCTACCCCAAGTAGGAAAGATGGGATGATAGGATGTCAGCA 140
Qy 23 MetIleProGlu 26
Db 141 ATAATACCAGAA 152
RESULT 9
BI926735/c
LOCUS BI926735 642 bp mRNA linear EST 18-OCT-2001
DEFINITION EST546624 tomato flower, buds 0-3 mm Lycopersicon esculentum cDNA clone CTOA30F5 5' end, mRNA sequence.
ACCESSION BI926735
VERSION BI926735.1 GI:16235507
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 642)
REFERENCE van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, 0-3 mm buds (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

FEATURES

source
Seq primer: T3.
Location/Qualifiers
1. .642
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTOA30F5"
/tissue_type="flower"
/dev_stage="0-3mm buds"
/clone_lib="tomato flower, buds 0-3 mm"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

Alignment Scores:
Pred. No.: 0.00122 Length: 642
Score: 88.00 Matches: 15
Percent Similarity: 87.50% Conservative: 6
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 59.86% Indels: 0
DB: 4 Gaps: 0

ORIGIN

US-10-014-101B-32 (1-28) x BI926735 (1-642)
QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 630 AATGGACCCATACCTTGTCTACCAAGTAGGAAAGATGGGATGATAGGATGCAGCA 571
QY 23 MetIleProGlu 26
Db 570 ATAATACCAGAA 559

RESULT 10
CO119329/c

LOCUS
DEFINITION
GR_Eb022C22.f GR_Eb Gossypium raimondii cDNA clone GR_Eb022C22 5', mRNA sequence.
CO119329
CO119329.1 GI:48818016
EST.
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (bases 1 to 757)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 022 row: C column: 22.

FEATURES

source
Location/Qualifiers
1. .757
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Eb022C22"
/tissue_type="floral"

Alignment Scores:
Pred. No.: 0.00159 Length: 795
Score: 88.00 Matches: 15

ORIGIN

US-10-014-101B-32 (1-28) x CO119329 (1-757)
QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 545 ACAGGCCCTGTCTCGTTATCTCTATGAACACACACAAAAGTGGATGATAGGATGTCAGCT 486
QY 23 MetIleProGlu 26
Db 485 GTAATACCAGAT 474

RESULT 11

CO117913/c

LOCUS
DEFINITION
CO117913
CO117913.1 GI:48816600
EST.
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (bases 1 to 795)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 01 row: P column: 23.

FEATURES

source
Location/Qualifiers
1. .795
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Eb01P23"
/tissue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_Eb"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

/dev_stage="3 to +3 DPA"

/lab_host="DH10B"

/clone_lib="GR_Eb"

/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Alignment Scores:
Pred. No.: 0.00149 Length: 757
Score: 88.00 Matches: 15
Percent Similarity: 83.33% Conservative: 5
Best Local Similarity: 62.50% Mismatches: 4
Query Match: 59.86% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-32 (1-28) x CO119329 (1-757)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22

Db 545 ACAGGCCCTGTCTCGTTATCTCTATGAACACACACAAAAGTGGATGATAGGATGTCAGCT 486

QY 23 MetIleProGlu 26

Db 485 GTAATACCAGAT 474

Percent Similarity: 83.33% Conservative: 5
Best Local Similarity: 62.50% Mismatches: 4
Query Match: 59.86% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-32 (1-28) x CO117913 (1-795)

Qy 3 SerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 518 ACAGGACCTGTCCTCGTTTATCCTATGAACAGACACAAAAGTGGGATGATGATGTCAGCT 459

Qy 23 MetIleProGlu 26

Db 458 GTAATACCAGAT 447

RESULT 12

CA766652

LOCUS

DEFINITION

CA766652 807 bp mRNA linear EST 08-JAN-2003
AF53-Rpf 12_E14_T7_051.abi IRRI Drought Stress Panicle Library
Oryza sativa (indica cultivar-group) cDNA clone C0004334 5', similar
to Hypothetical 47.9 kDa oxidoreductase in fasciation locus (ORF5),
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bennett,J., Arumugam,K., Lafitte,R., Wen,J., Rudd,S. and
Bruskiewich,R.M.

IRRI Drought Stress Panicle cDNA Library

Unpublished (2002)

On Dec 2, 2002 this sequence version replaced gi:25995907.

Contact: Richard Bruskiewich

Biometrics and Bioinformatics Unit

International Rice Research Institute

DAPO 7777, Metro Manila, Philippines

Tel: +63-2-845-0563

Fax: +63-2-845-0606

Email: r.bruskiewich@cgiar.org

International Rice Information System (IRIS;

<http://www.iris.irri.org>): D0204333

Assignment of putative function to the sequence by S. Rudd of the

Munich Information Center for Protein Sequences

(<http://mips.gsf.de>)

Plate: 12 row: E column: 14.

Location/Qualifiers

1. .807

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="mRNA"

/cultivar="IR64"

/db_xref="taxon:39946"

/clone="C0004334"

/tissue_type="Panicles"

/dev_stage="Flowering"

/clone_lib="IRRI Drought Stress Panicle Library"

/note="Vector: pBluescript II SK+; Water stress was

applied by not watering for 4 consecutive days. Panicles

were collected from control (well watered) and stressed

plants at 2 days before heading, at heading, 50% flowering

and 4 days after 50% flowering."

ORIGIN

Alignment Scores:

Pred. No.:

Score: 0.00161

Percent Similarity: 88.00

Best Local Similarity: 73.08%

Query Match: 61.54%

DB: 59.86%

Length: 807

Matches: 16

Conservative: 3

Mismatches: 7

Indels: 0

Gaps: 0

US-10-014-101B-32 (1-28) x CA766652 (1-807)

Qy 1 SerAlaSerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMet 20
Db 532 AGCAACAATGGTCCCATCTGCTTTACCCAGTGAACAGAACCAAGTGGGACACAGACA 591

Qy 21 SerAlaMetIleProGlu 26

Db 592 TCAGTGGTCATACCAGAT 609

RESULT 13

CO121610

LOCUS

DEFINITION

CO121610 824 bp mRNA linear EST 16-JUN-2004
GR_Eb02N24.f GR_Eb Gossypium raimondii cDNA clone GR_Eb02N24 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CO121610.1 GI:48820297
EST.
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE

AUTHORS

Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.

Global assembly of Cotton ESTs

Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ, 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: <http://genome.arizona.edu>

Plate: 02 row: N column: 24.

Location/Qualifiers

1. .824

/organism="Gossypium raimondii"

/mol_type="mRNA"

/db_xref="taxon:29730"

/clone="GR_Eb02N24"

/tissue_type="floral"

/dev_stage="3 to +3 DPA"

/lab_host="DH10B"

/clone_lib="GR_Eb"

/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:

EcoRV; Library made by Invitrogen with RNA supplied by

Wendle lab. Directional cloned into NotI-EV. Colonies

plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Alignment Scores:

Pred. No.:

Score: 0.00166

Percent Similarity: 88.00

Best Local Similarity: 83.33%

Query Match: 62.50%

DB: 59.86%

Length: 824

Matches: 15

Conservative: 5

Mismatches: 4

Indels: 0

Gaps: 0

US-10-014-101B-32 (1-28) x CO121610 (1-824)

Qy 3 SerGlyLeuAlaLeuLeuTyProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
Db 735 ACAGGACCTGTCCTCGTTTATCCTATGAACAGACACAAAAGTGGGATGATGATGTCAGCT 794

Qy 23 MetIleProGlu 26

Db 795 GTAATACCAGAT 806

RESULT 14

CL960490
LOCUS
DEFINITION
OSIFCC004596 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL960490
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 1578)
AUTHORS
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL
COMMENT
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
Location/Qualifiers
1..1578
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "
ORIGIN
Alignment Scores:
Pred. No.: 0.00368 Length: 1578
Score: 88.00 Matches: 16
Percent Similarity: 73.08% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 7
Query Match: 59.86% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-32 (1-28) x CL960490 (1-1578)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
||| :|||
Db 1210 AGCAACAATGGTCCCATACTGCTTTACCCAGTGAACAGAACCAAGTGGGACAACAGACA 1269
QY 21 SerAlaMetIleProGlu 26
||| :|||
Db 1270 TCAGTGGTCATACCAGAT 1287
RESULT 15
CB620527
LOCUS
DEFINITION
CB620527 772 bp mRNA linear EST 08-APR-2003
OSIIEa05N03.f OSIIEa Oryza sativa (indica cultivar-group) cDNA clone OSIIEa05N03 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 772)
AUTHORS
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE
Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

JOURNAL
COMMENT
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: N column: 03
Seq primer: gta aaa cga cgg cca gtg.
FEATURES
source
Location/Qualifiers
1..772
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIIEa05N03"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIEa"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Lesion Mimic SPL 11"
ORIGIN
Alignment Scores:
Pred. No.: 0.00222 Length: 772
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservative: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-32 (1-28) x CB620527 (1-772)
QY 2 AlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
||| :|||
Db 498 GCCATGGGCCCGTCCTCATCTACCCCATGAACCGCAACAAAGTGGGACAGTAACATGTCG 557
QY 22 AlaMetIleProGluIleAsp 28
||| :|||
Db 558 GCAGTGATCACCGACGACGAC 578
RESULT 16
CO435706
LOCUS
DEFINITION
CO435706 863 bp mRNA linear EST 01-OCT-2004
OSMR772 5MT resistant rice mutant cDNA library Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 863)
AUTHORS
Kim,D.S., Lee,I.S., Kang,S.Y., Song,H.S., Lee,Y.I. and Seo,Y.W.
TITLE
Expressed sequence tag (EST) analysis and characterization of differentially expressed genes related to 5-methyltryptophan (5MT) resistance in mutant rice
JOURNAL
COMMENT
Unpublished (2003)
Contact: Seo YW
Department of Crop Science, division of Biotechnology and Genetic Engineering
Korea University
Anam-Dong, Seongbuk-Gu, Seoul, 136-701, Korea
Tel: +82 2 3290 3005
Fax: +82 2 3290 3501

FEATURES source
Email: seoag@korea.ac.kr.
Location/Qualifiers
1. .863
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Donganbyeon"
/db_xref="taxon:39947"
/tissue_type="5MT treated leaves, stems, and roots"
/dev_stage="seedling grown for 3 weeks"
/lab_host="XLI-Blue MRF"
/clone_lib="5MT resistant rice mutant cDNA library"
/note="Vector: pBluescripts SK(+/+) phagemid; The rice mutant resistant to growth inhibition by 5MT were selected from the callus irradiated with gamma ray of 50 Gy through rice cv. Donganbyeon embryo culture. For construction of the cDNA library, 5MT resistant homologous rice mutants were treated by 5MT for 3 weeks."

ORIGIN
Alignment Scores:
Pred. No.: 0.00254 Length: 863
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservativeness: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-32 (1-28) x CO435706 (1-863)

Qy 2 AlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
Db 90 GCCATGGGCCCCGCTCTCATCTACCCATGAACCGCAACAGTGGGACAGTAACATGTCG 149

Qy 22 AlaMetIleProGluIleAsp 28
Db 150 GCAGTGATCACCGACGACGAC 170

RESULT 17
CL957466
LOCUS 1671 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC000646 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL957466
VERSION CL957466.1 GI:52369841
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 1671)
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1. .1671
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Alignment Scores:
Pred. No.: 0.00572 Length: 1671
Score: 87.00 Matches: 16
Percent Similarity: 74.07% Conservativeness: 4
Best Local Similarity: 59.26% Mismatches: 7
Query Match: 59.18% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x CL957466 (1-1671)

Qy 2 AlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSer 21
Db 1312 GCCATGGGCCCCGCTCTCATCTACCCATGAACCGCAACAGTGGGACAGTAACATGTCG 1371

Qy 22 AlaMetIleProGluIleAsp 28
Db 1372 GCAGTGATCACCGACGACGAC 1392

RESULT 18
AU227876/c
LOCUS 436 bp mRNA linear EST 23-APR-2002
DEFINITION AU227876 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-29-H04 3', mRNA sequence.
ACCESSION AU227876
VERSION AU227876.1 GI:19742523
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 436)
AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
TITLE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
Location/Qualifiers
1. .436
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-29-H04"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: Sali"

FEATURES source
Location/Qualifiers
1. .436
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-29-H04"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: Sali"

ORIGIN
Alignment Scores:
Pred. No.: 0.00133 Length: 436
Score: 86.50 Matches: 18
Percent Similarity: 80.00% Conservativeness: 2
Best Local Similarity: 72.00% Mismatches: 4
Query Match: 58.84% Indels: 1
DB: 1 Gaps: 1

```
US-10-014-101B-32 (1-28) x AU227876 (1-436)

QY      4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      431 GGACTCGCTGTTCTCTATCCAAACAACCGGAATAATGGACAATCTATGTC---GGCATG 375

QY      24 IleProGluIleAsp 28
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      374 ATACCAGAGATCGAT 360

RESULT 19
BG518327
LOCUS   BG518327
DEFINITION BG518327 438 bp mRNA linear EST 02-APR-2001
sequence.
ACCESSION BG518327
VERSION   BG518327.1 GI:13516051
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM  Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 438)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL   University
COMMENT   Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 947066 row: A column: 06.
Location/Qualifiers
1. .438
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab_host="XL1-Blue"
/clone_lib="947 - 2 week shoot from Barkan lab"
/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
Site 1: EcoRI; Site 2: XhoI; Directionally cloned using
Stratagene's Unizap_XR cDNA cloning kit with the 5' end
at the EcoRI site. The library represents 8 x 10e5
independent recombinant phage. The plants were greenhouse
grown."

ORIGIN
Alignment Scores:
Pred. No.: 0.00161 Length: 438
Score: 86.00 Matches: 15
Percent Similarity: 76.92% Conservatave: 5
Best Local Similarity: 57.69% Mismatches: 6
Query Match: 58.50% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x BG518327 (1-438)

QY      1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMet 20
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      228 AGCAACAATGGTCCCATATTGCTTATCCAGTGAACAATCAAAGTGGGACAACAGAACG 287

QY      21 SerAlaMetIleProGlu 26
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      288 TCAGTAGTCATACCATGAT 305
```

```
RESULT 20
BI203744
LOCUS   BI203744
DEFINITION BI203744 642 bp mRNA linear EST 11-JUL-2001
sequence.
ACCESSION BI203744
VERSION   BI203744.1 GI:14681468
KEYWORDS  EST.
SOURCE    Lycopersicon esculentum (tomato)
ORGANISM  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 642)
van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R.,
Ronning,C. and Tanksley,S.
Generation of ESTs from Tomato Suspension Cultures
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. .642
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496, E6203"
/db_xref="taxon:4081"
/clone="cTOS2N10"
/tissue_type="suspension cultures"
/lab_host="SOLR"
/clone_lib="cTOS"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
shaking."

ORIGIN
Alignment Scores:
Pred. No.: 0.00257 Length: 642
Score: 86.00 Matches: 15
Percent Similarity: 83.33% Conservatave: 5
Best Local Similarity: 62.50% Mismatches: 4
Query Match: 58.50% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-32 (1-28) x BI203744 (1-642)

QY      3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
      ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      114 ACTGGACCCATACCTTGCTACCCCAACCAAGTCGGAAAGATGGGATGATAGGATGTCAGCC 173

QY      23 MetIleProGlu 26
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      174 ACGATACCAGAA 185

RESULT 21
BI204708
LOCUS   BI204708
DEFINITION BI204708 715 bp mRNA linear EST 11-JUL-2001
sequence.
ACCESSION BI204708
VERSION   BI204708.1 GI:14682432
KEYWORDS  EST.
SOURCE    Lycopersicon esculentum (tomato)
ORGANISM  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
```


Alignment Scores:
Pred. No.: 0.00392 Length: 906
Score: 86.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 58.50% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x CG289642 (1-906)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 672 GCCGGGATCATCTCATGTACCCCATGAACAGGACAGGTGGGACCGGATGACAGCG 613

QY 23 MetIleProGluIleAsp 28
|||||
Db 612 ATGACCCCGACGCCACGGAC 595

RESULT 24
CG351153/c
LOCUS
DEFINITION
CG351153 963 bp DNA linear GSS 26-AUG-2003
genomic survey sequence.
ACCESSION
CG351153
VERSION
CG351153.1 GI:34268419
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 963)
AUTHORS
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
CONSORTIUM for Maize Genomics
Unpublished (2002)
Other_GSSs: OG2BM20TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1. .963
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0753D15"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0:7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 0.00422 Length: 963
Score: 86.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 58.50% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-32 (1-28) x CG351153 (1-963)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 487 GCCGGGATCATCTCATGTACCCCATGAACAGGACAGGTGGGACCGGATGACAGCG 428

QY 23 MetIleProGluIleAsp 28
|||||
Db 427 ATGACCCCGACGCCACGGAC 410

RESULT 25
CB913923
LOCUS
DEFINITION
CB913923 584 bp mRNA linear EST 25-APR-2003
VVD172F06 377903 An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
cDNA clone VVD172F06 5, mRNA sequence.

ACCESSION
CB913923
VERSION
CB913923.1 GI:30128584
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
REFERENCE
1 (bases 1 to 584)
AUTHORS
Cushman,J.C.
TITLE
An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 172 row: F column: 06
Seq primer: T3 20mer
High quality sequence stop: 584.
Location/Qualifiers
1. .584
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD172F06"
/tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 0.00331 Length: 584
Score: 85.00 Matches: 15
Percent Similarity: 73.08% Conservative: 4
Best Local Similarity: 57.69% Mismatches: 7
Query Match: 57.82% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-32 (1-28) x CB913923 (1-584)

QY 3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22
|||||
Db 97 AGTGGCCCCATCCTCATCTACCTATGAACAAAAACAAGTGGGACCGCACATCGGTG 156

QY 23 MetIleProGluIleAsp 28
:::|||||
Db 157 GTTACGCCAGAGGAGGAC 174

RESULT 26
CF210007/c
LOCUS
DEFINITION
CF210007 741 bp mRNA linear EST 01-AUG-2003
CAB20005 IVb_Rb_G06 Cabernet Sauvignon Flower bloom - CAB2 Vitis
vinifera_cDNA clone CAB20005_IVb_Rb_G06 3', mRNA sequence.

US-10-014-101B-32 (1-28) x BI970438 (1-773)	
QY	4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23 :::
Db	684 GGACCACTCTGGTTATCCCATGAATAGAAACAAGTGGTACGATAGGATGTCAGCATCT 625
QY	24 IleProGluIleAsp 28 :::
Db	624 ATACCAGACGAGGAT 610
RESULT 28	
CF209921	
LOCUS	CF209921 809 bp mRNA linear EST 01-AUG-2003
DEFINITION	CAB20005_IVb_Fb_G06 Cabernet Sauvignon Flower bloom - CAB2 Vitis
ACCESSION	vinifera_cDNA clone CAB20005_IVb_Fb_G06 5', mRNA sequence.
VERSION	CF209921
KEYWORDS	CF209921.1 GI:33404294
SOURCE	EST.
ORGANISM	Vitis vinifera
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE	rosids; Vitaceae; Vitis.
JOURNAL	1 (bases 1 to 809)
COMMENT	Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J., Jones,K. and Cook,D. Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages Unpublished (2003) Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drook@ucdavis.edu Seq primer: ACGTACCGACATATGCC.
FEATURES	Location/Qualifiers
source	1..809
	/organism="Vitis vinifera"
	/mol_type="mRNA"
	/cultivar="Cabernet Sauvignon"
	/db_xref="taxon:29760"
	/clone="CAB20005_IVb_Fb_G06"
	/sex="Hermaphrodite"
	/dev_stage="Bloom"
	/clone_lib="Cabernet Sauvignon Flower bloom - CAB2"
	/note="Organ: Flower - Bloom; Vector: pDNR; Site_1: Sfil; Site_2: Sfil; CAB2 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 berries. Samples were collected at full bloom (80 to 100% flowers showing dehiscence of calyptras or caps and anthers fully extended). Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGGTATCAACGACAGAGTGCGCCATTACGCCGGG-3' and 5'-ATTCTAGAGCGGAGCGGCGGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."
ORIGIN	
Alignment Scores:	
Pred. No.:	0.00494 Length: 809
Score:	85.00 Matches: 15
Percent Similarity:	73.08% Conservative: 4
Best Local Similarity:	57.69% Mismatches: 7
Query Match:	57.82% Indels: 0
DB:	7 Gaps: 0
US-10-014-101B-32 (1-28) x CF209921 (1-809)	
QY	3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 22

Db	404 AGTGGCCCCATCCTCATCTACCTATGACAAACAAAGTGGGACGACCATCGGTG 463 :::
QY	23 MetIleProGluIleAsp 28 :::
Db	464 GTTACGCCAGAGGAGGAC 481
RESULT 29	
CL964867	
LOCUS	CL964867 1587 bp DNA linear GSS 21-SEP-2004
DEFINITION	OsIFCC011216 Oryza sativa Express Library Oryza sativa (indica
ACCESSION	cultivar-group) genomic, genomic survey sequence.
VERSION	CL964867
KEYWORDS	CL964867.1 GI:52384422
SOURCE	GSS.
ORGANISM	Oryza sativa (indica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE	Ehrhartoideae; Oryzeae; Oryza.
JOURNAL	1 (bases 1 to 1587)
COMMENT	Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis Unpublished (2004) Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559 Fax: 86-10-80488676 Email: chenchen@genomics.org.cn Rice genomic sequence. Class: exon-trapped.
FEATURES	Location/Qualifiers
source	1..1587
	/organism="Oryza sativa (indica cultivar-group)"
	/mol_type="genomic DNA"
	/db_xref="taxon:39946"
	/clone_lib="Oryza sativa Express Library"
	/note="Oryza sativa exon trapped genomic sequences"
ORIGIN	
Alignment Scores:	
Pred. No.:	0.0113 Length: 1587
Score:	85.00 Matches: 14
Percent Similarity:	80.00% Conservative: 6
Best Local Similarity:	56.00% Mismatches: 5
Query Match:	57.82% Indels: 0
DB:	9 Gaps: 0
US-10-014-101B-32 (1-28) x CL964867 (1-1587)	
QY	4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23 :::
Db	1255 GGCCTCATCCTCATGTACCCCATGAATAAGGACATGTGGGATGACAGGATGACGGCGATG 1314
QY	24 IleProGluIleAsp 28 :::
Db	1315 AGCCGGACGAGGAC 1329
RESULT 30	
CO174423/c	
LOCUS	CO174423 757 bp mRNA linear EST 18-JUN-2004
DEFINITION	NDL1_43_H11_A029 Needles control Pinus taeda cDNA clone
ACCESSION	NDL1_43_H11_A029 5', mRNA sequence.
VERSION	CO174423
KEYWORDS	CO174423.1 GI:48947295
SOURCE	EST.
ORGANISM	Pinus taeda (loblolly pine)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 757)
 Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and
 Dean, J.F.D.
 An EST database from untreated loblolly pine (Pinus taeda) needles
 Unpublished (2004)
 Other_ESTs: NDL1_43_H11.b1_A029
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 RNA prepared and library constructed by W. Walter Lorenz (School of
 Forest Resources, University of Georgia); plant material prepared
 by Craig Zimmermann (School of Forest Resources, University of
 Georgia) using rooted cuttings provided by the Forest Biology
 Research Cooperative (FBRC) and the CCLONES project at the
 University of Florida; sequencing done in the Laboratory for
 Genomics and Bioinformatics, University of Georgia. Sequence ends
 have been trimmed to exclude vector and regions below Phred quality
 16. Three-prime sequences are presented as their reverse complement
 and have been trimmed to exclude polyA.
 Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
 source

1..757
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="3 CCLONES"
 /db_xref="taxon:3352"
 /clone="NDL1_43_H11_A029"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Needles control"
 /note="Organ: needle; Vector: pSL1180; Site 1: EcoRI;
 Site 2: XhoI; The library was prepared from polyA+ RNA
 from the needles of 1-year-old loblolly pine (Pinus taeda)
 cuttings that were rooted and then planted in washed sand.
 Just before harvesting needles for RNA isolation, the
 rooted cuttings were maintained for 27 days (April 2003)
 under ambient conditions in a local greenhouse. They were
 kept on a weekly regimen of 0.5x nutrient-complete
 Hoagland's solution and supplemented with additional water
 sufficient to maintain a 15% soil moisture content.
 Double-stranded cDNA was cloned unidirectionally into
 pSL1180. Inserts can be excised with EcoRI (5' end) and
 XhoI (3' end)."
 Alignment Scores:
 Pred. No.: 0.00661 Length: 757
 Score: 84.00 Matches: 15
 Percent Similarity: 73.91% Conservative: 2
 Best Local Similarity: 65.22% Mismatches: 6
 Query Match: 57.14% Indels: 0
 DB: 7 Gaps: 0
 US-10-014-101B-32 (1-28) x CO174423 (1-757)
 QY 4 GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMet 23
 Db 674 GGACCCATGCTCCTATATCCTCTGAACAGAAACAGTGGGATTGTCGTATGCTACAGCA 615
 QY 24 IleProGlu 26
 Db 614 GTGCCCGAT 606
 RESULT 31
 CO174338/c
 LOCUS
 DEFINITION
 NDL1_43_H11_A029 3', mRNA sequence.

RESULT 32
AV536711
LOCUS
DEFINITION AV536711 Arabidopsis thaliana liquid-cultured seedlings Columbia EST 20-FEB-2004
Arabidopsis thaliana cDNA clone PAZNII0455R 5', mRNA sequence.
ACCESSION AV536711
VERSION AV536711.1 GI:8696994
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 481)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
20363093
10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
source
1..481
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="PAZNII0455R"
/tissue type="liquid-cultured seedlings"
/clone_lib="Arabidopsis thaliana liquid-cultured seedlings
Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
ORIGIN
Alignment Scores:
Pred. No.: 0.00549 Length: 481
Score: 83.00 Matches: 19
Percent Similarity: 37.93% Conservative: 3
Best Local Similarity: 32.76% Mismatches: 6
Query Match: 56.46% Indels: 30
DB: 1 Gaps: 1
US-10-014-101B-32 (1-28) x AV536711 (1-481)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 15
Db 209 TCAACTTCTGGTGTACTCTCTCTATCCCAACCGAACAAGTAAATATTACTTTT 268
QY 15 ----- 15
Db 269 TGATTTTGTATTATTGAAAGTATATCCCAATAATGTATGTTAAATTGTTAACAGAATT 328
QY 16 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAsp 28
Db 329 TATTTTATTAATAGATGGAACACCGCATGTCAACGATGACACCGGACGAAGAT 382
RESULT 33
CL947867
LOCUS
DEFINITION CL947867 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION CL947867
VERSION CL947867.1 GI:52359876
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1566)
Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..1566
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "
ORIGIN
Alignment Scores:
Pred. No.: 0.0234 Length: 1566
Score: 83.00 Matches: 14
Percent Similarity: 76.92% Conservative: 6
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 56.46% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-32 (1-28) x CL947867 (1-1566)
QY 1 SerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAsnArgMet 20
Db 1201 AGTAAACAATGGTCCCATATTACTCTATCCAGTGAACAAATCCAGATGGGACAGAAC 1260
QY 21 SerAlaMetIleProGlu 26
Db 1261 TCAGTAGTCATACCCAGAT 1278
RESULT 34
BF520835
LOCUS
DEFINITION BF520835 DSIL Medicago truncatula cDNA clone pDSIL-39F7, mRNA
sequence.
ACCESSION BF520835
VERSION BF520835.1 GI:11609518
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 575)
Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S.,
Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B.,
Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTs from leaves of Medicago truncatula after inoculation with
Colletotrichum trifolii
Unpublished (2000)
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058


```
DB:              7              Gaps:              0
US-10-014-101B-32 (1-28) x CO485966 (1-856)
QY      3 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMetSerAla 22
Db      406 AATGGATTAAATGCTCCTGTATCCTCTGAAGAAAAGCTTGTGGGATTCTCGCACGTCCGCT 347
QY      23 MetIleProGluIleAsp 28
Db      346 GTTATTCCAGAGGAGGAT 329
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Search completed: February 18, 2005, 14:07:05
Job time : 7208 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2005, 21:59:48 ; Search time 959.84 Seconds
(without alignments)
353.378 Million cell updates/sec

Title: US-10-014-101B-39
Perfect score: 35
Sequence: 1 VGGTSLN 7

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2 1/USPTO spool/US10014101/runat 16022005 075845 7936/app query.fasta 1.796
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_htg:*
3: gb_in:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	116	11 BX295789	BX295789 Arabidops
2	35	100.0	379	8 AY444352	AY444352 Pisum sat
3	35	100.0	424	11 BX323242	BX323242 Arabidops
4	35	100.0	442	6 AX886741	AX886741 Sequence

C	5	35	100.0	442	6	BD026351	Sequence
	6	35	100.0	1506	6	CQ812637	Sequence
	7	35	100.0	1506	6	AX339729	Sequence
	8	35	100.0	1506	6	AX785077	Sequence
	9	35	100.0	1515	6	AX339733	Sequence
	10	35	100.0	1515	6	AX785081	Sequence
	11	35	100.0	1537	8	BT005653	Arabidops
	12	35	100.0	1566	6	AX654568	Sequence
	13	35	100.0	1572	6	AX339730	Sequence
	14	35	100.0	1572	6	AX785078	Sequence
	15	35	100.0	1572	8	AF303979	Arabidops
	16	35	100.0	1575	6	AX339731	Sequence
	17	35	100.0	1575	6	AX507394	Sequence
	18	35	100.0	1575	6	AX651615	Sequence
	19	35	100.0	1575	6	AX785079	Sequence
	20	35	100.0	1575	8	AF303980	Arabidops
	21	35	100.0	1575	8	AF303981	Arabidops
	22	35	100.0	1587	6	AX653027	Sequence
	23	35	100.0	1590	6	AX653226	Sequence
	24	35	100.0	1593	6	AX652883	Sequence
	25	35	100.0	1605	6	AR150952	Sequence
	26	35	100.0	1605	6	AR399211	Sequence
	27	35	100.0	1606	8	BT002757	Arabidops
	28	35	100.0	1608	6	AX039923	Sequence
	29	35	100.0	1611	6	AX339732	Sequence
	30	35	100.0	1611	6	AX785080	Sequence
	31	35	100.0	1620	6	AX339737	Sequence
	32	35	100.0	1620	6	AX785085	Sequence
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	34	35	100.0	1655	8	BT000179	Arabidops
	35	35	100.0	1677	6	AX653630	Sequence
	36	35	100.0	1687	8	BT004107	Arabidops
	37	35	100.0	1728	6	CQ812635	Sequence
	38	35	100.0	1728	6	AX339728	Sequence
	39	35	100.0	1728	6	AX785076	Sequence
	40	35	100.0	1776	8	ZMY18377	Sequence
	41	35	100.0	1857	8	AF540382	Hordeum v
	42	35	100.0	1863	8	AY054460	Arabidops
	43	35	100.0	1866	8	AY209184	Hordeum v
	44	35	100.0	1873	8	AY091158	Arabidops
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ALIGNMENTS

RESULT 1	BX295789	116 bp	DNA	linear	STS 11-JUN-2003
LOCUS	Arabidopsis thaliana	transposon insertion	STS SM_3.33583,	sequence	
DEFINITION	tagged site.				
ACCESSION	BX295789				
VERSION	BX295789.1	GI:29169627			
KEYWORDS	STS; STS, sequence tagged site.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi				
REFERENCE	1				
AUTHORS	Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B., Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 116)				
AUTHORS	Clarke,J.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK				
COMMENT	AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3'end of the transposon, _5 denotes a sequence derived from the 5'end of the				

transposon BBSRC GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N120294.

FEATURES
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Location/Qualifiers
1..116
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/db_xref="taxon:3702"
/clone="AL079344"
/note="Derived from superpool 1.32 NASC code N40031"
1..116
/standard_name="SM_3.33583"

STS

ORIGIN

Alignment Scores:
Pred. No.: 78.9 Length: 116
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-39 (1-7) x BX295789 (1-116)

QY 1 ValGlyGlyThrLeuSerAsn 7
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Db 80 GTCGGCGGACGTTGTCGAAC 100

RESULT 2
AY444352/c
LOCUS AY444352 379 bp DNA linear PLN 16-DEC-2003
DEFINITION Pisum sativum cytokinin oxidase/dehydrogenase 1 (PCKX1) gene,
partial sequence.
ACCESSION AY444352
VERSION AY444352.1 GI:39636914
KEYWORDS
SOURCE Pisum sativum (pea)
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.

REFERENCE 1 (bases 1 to 379)
AUTHORS Vaseva-Gemisheva,I.I., Lee,D., Turner,L., Ellis,N. and Karanov,E.N.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-2003) Plant Physiology Institute, Bulgarian
Academy of Sciences, Georgi Bonchev 21 Building, Sofia 1113,
Bulgaria

FEATURES
source
Location/Qualifiers
1..379
/organism="Pisum sativum"
/mol_type="genomic DNA"
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/chromosome="6"
/tissue type="leaves"
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/gene="PCKX1"
/note="cytokinin oxidase/dehydrogenase 1"

gene

ORIGIN

Alignment Scores:
Pred. No.: 214 Length: 379
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x AY444352 (1-379)

QY 1 ValGlyGlyThrLeuSerAsn 7

|||||
Db 160 GTGGGTGAACGCTCTCTAAC 140

RESULT 3
BX323242
LOCUS BX323242 424 bp DNA linear STS 10-JUN-2003
DEFINITION Arabidopsis thaliana transposon insertion STS SM_3.38194, sequence
tagged site.
ACCESSION BX323242
VERSION BX323242.1 GI:29602993
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,
Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 424)
AUTHORS Clarke,J.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2003) Clarke J.H., John Innes Centre, Colney
lane, Norwich, NR4 7UJ, UK

COMMENT
AT denotes an activation tag dissociation transposon within a
single line, Et an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. _3 denotes a sequence derived from the 3'end of the
transposon, _5 denotes a sequence derived from the 5'end of the
transposon BBSRC GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N124905.

FEATURES
source
Location/Qualifiers
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/note="Derived from superpool 15.46 NASC code N40693"
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/standard_name="SM_3.38194"

STS

ORIGIN

Alignment Scores:
Pred. No.: 235 Length: 424
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-39 (1-7) x BX323242 (1-424)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 365 GTTGAGGTACACTCTCCAAT 385

RESULT 4
AX886741/c
LOCUS AX886741 442 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2604 from Patent EP1033401.
ACCESSION AX886741
VERSION AX886741.1 GI:40044205
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.

TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 2604 06-SEP-2000;
Genset (FR)

FEATURES
source Location/Qualifiers
1..442

CDS
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/mol_type="unassigned DNA"
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126..>440
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EVE"

ORIGIN

Alignment Scores: 243 Length: 442
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-014-101B-39 (1-7) x AX886741 (1-442)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 67 GTGGGCGGAACGCTTTCTAAT 47

RESULT 5

BD026351/c
LOCUS BD026351 442 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD026351
VERSION BD026351.1 GI:22567574
KEYWORDS JP 2001269182-A/2597.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 2597 02-OCT-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/2597
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers
FT CDS 126..440.

FEATURES
source Location/Qualifiers
1..442

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/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 243 Length: 442
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Score: 100.00% Conservative: 0
Percent Similarity:

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x BD026351 (1-442)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 67 GTGGGCGGAACGCTTTCTAAT 47

RESULT 6

CQ812637
LOCUS CQ812637 1506 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 3 from Patent WO2004038027.
ACCESSION CQ812637
VERSION CQ812637.1 GI:47602086
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE

1 van Camp,W.
AUTHORS Bioremediation
TITLE Patent: WO 2004038027-A 3 06-MAY-2004;
JOURNAL CropDesign N.V. (BE)
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores: 682 Length: 1506
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Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-014-101B-39 (1-7) x CQ812637 (1-1506)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGAGGAACGTTGTCGAAT 486

RESULT 7

AX339729
LOCUS AX339729 1506 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 26 from Patent WO0196580.
ACCESSION AX339729
VERSION AX339729.1 GI:18135722
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE

1 Schmulling,T. and Werner,T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 0196580-A 26 20-DEC-2001;
JOURNAL Schmulling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES Location/Qualifiers
1..1506
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:

Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
Ecker,J.R. and Theologis,A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 1537)
Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,
Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
Ecker,J.R. and Theologis,A.
Direct Submission
Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,
Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M.,
Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome
submitted to Genbank.

FEATURES
source

Location/Qualifiers
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/note="This clone is in PUNI 51."
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/product="putative cytochrome oxidase"
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/translation="MANLRMTLITVLMITKSSNGIKIDLPKSLNLTSTDPISIISA
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SNGVIGGQVFRNGPLVSNVLELDVITKGEMLTCSRQLNPFLFYGVGLGLGQFGIITR
ARIVLDHAPKRAKWFRLYSDFTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTS
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/gene="At2g19500"

3'UTR

ORIGIN

Alignment Scores:
Pred. No.: 694 Length: 1537
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x BT005653 (1-1537)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGGAGGAACTGTTCGAAT 486

RESULT 12

AX654568

LOCUS

AX654568 Sequence 4438 from Patent WO03000898.

DEFINITION

AX654568

ACCESSION

AX654568.1 GI:29157382

VERSION

KEYWORDS

Oryza sativa

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1

AUTHORS

Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.

TITLE

Plant genes involved in defense against pathogens

JOURNAL

Patent: WO 03000898-A 4438 03-JAN-2003;

SYNGENTA PARTICIPATIONS AG (CH)

FEATURES

Location/Qualifiers
1..1566
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN

Alignment Scores:
Pred. No.: 705 Length: 1566
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX654568 (1-1566)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 499 GTTGGAGGCACACTGTTCGAAT 519

RESULT 13

AX339730

LOCUS

AX339730 Sequence 27 from Patent WO0196580.

DEFINITION

AX339730

ACCESSION

AX339730.1 GI:18135723

VERSION

KEYWORDS

Arabidopsis thaliana (thale cress)

SOURCE

Arabidopsis thaliana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

1

AUTHORS

Schmueling,T. and Werner,T.

TITLE

Method for modifying plant morphology, biochemistry and physiology

JOURNAL

Patent: WO 0196580-A 27 20-DEC-2001;

SYNGENTA PARTICIPATIONS AG (DE)

FEATURES

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/mol_type="unassigned DNA"
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VERSION	AX785078.1	GI:32952909	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Schmulling, T. and Werner, T.		
TITLE	Method for modifying plant morphology, biochemistry and physiology		
JOURNAL	Patent: WO 03050287-A 27 19-JUN-2003;		
FEATURES	Schmulling, Thomas (DE) ; Werner, Tomas (DE)		
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ACCESSION	AF303979		PLN 08-NOV-2000
VERSION	AF303979.1	GI:11120509	
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SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
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AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1572)		
AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA		
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AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
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AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA		
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VERSION	AF303979.1	GI:11120509	
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AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1572)		
AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA		
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ACCESSION	AF303979		PLN 08-NOV-2000
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VERSION	AF303979.1	GI:11120509	
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ACCESSION	AF303979		PLN 08-NOV-2000
VERSION	AF303979.1	GI:11120509	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1572)		
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JOURNAL	Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA		
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ACCESSION	AF303979		PLN 08-NOV-2000
VERSION	AF303979.1	GI:11120509	
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ORGANISM	Arabidopsis thaliana		
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AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1572)		
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LOCUS	AF303979	1572 bp	mRNA
DEFINITION	Arabidopsis thaliana cytokinin oxidase (CKX3) mRNA, complete cds.		linear
ACCESSION	AF303979		PLN 08-NOV-2000
VERSION	AF303979.1	GI:11120509	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1572)		
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TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA		
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DEFINITION	Arabidopsis thaliana cytokinin oxidase (CKX3) mRNA, complete cds.		linear
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VERSION	AF303979.1	GI:11120509	
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ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	A family of cytokinin oxidases from Arabidopsis thaliana		
JOURNAL	Unpublished		
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AUTHORS	Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA		
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DEFINITION	Arabidopsis thaliana cytokinin oxidase (CKX3) mRNA, complete cds.		linear
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Db      535 GTCGGCGGGACGTTGTCGAAC 555

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DEFINITION      Sequence 2089 from Patent WO0216655.
ACCESSION      AX507394
VERSION      AX507394.1 GI:23388631
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1
AUTHORS      Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE      Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL      Patent: WO 0216655-A 2009 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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LOCUS      AX651615      1575 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION      Sequence 428 from Patent WO03000898.
ACCESSION      AX651615
VERSION      AX651615.1 GI:29154433
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1
AUTHORS      Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE      plant genes involved in defense against pathogens
JOURNAL      Patent: WO 03000898-A 428 03-JAN-2003;
Syngenta Participations AG (CH)
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QY      1 ValGlyGlyThrLeuSerAsn 7
Db      535 GTCGGCGGGACGTTGTCGAAC 555

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LOCUS      AX785079      1575 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Sequence 28 from Patent WO03050287.
ACCESSION      AX785079
VERSION      AX785079.1 GI:32952910
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1
AUTHORS      Schmulling, T. and Werner, T.
TITLE      Method for modifying plant morphology, biochemistry and physiology
JOURNAL      Patent: WO 03050287-A 28 19-JUN-2003;
Schmulling, Thomas (DE) ; Werner, Tomas (DE)
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QY      1 ValGlyGlyThrLeuSerAsn 7
Db      535 GTCGGCGGGACGTTGTCGAAC 555

RESULT 20
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LOCUS      AF303980      1575 bp      mRNA      linear      PLN 08-NOV-2000
DEFINITION      Arabidopsis thaliana cytokinin oxidase (CKX4) mRNA, complete cds.
ACCESSION      AF303980
VERSION      AF303980.1 GI:11120511
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 1575)
AUTHORS      Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and
Morris, R.O.
TITLE      A family of cytokinin oxidases from Arabidopsis thaliana
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1575)
AUTHORS      Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and
Morris, R.O.
TITLE      Direct Submission
JOURNAL      Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall,
Columbia, MO 65211, USA
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ORIGIN

Alignment Scores:
Pred. No.: 708 Length: 1575
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Query Match: 100.00% Indels: 0
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US-10-014-101B-39 (1-7) x AF303980 (1-1575)

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Db 535 GTCGGCGGGACGTTGTGGAAC 555

RESULT 21
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LOCUS Arabidopsis thaliana 1575 bp mRNA linear PLN 08-NOV-2000
DEFINITION Arabidopsis thaliana cytokinin oxidase (CKX5) mRNA, complete cds.
ACCESSION AF303981
VERSION AF303981.1 GI:11120513
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1575)
REFERENCE Bilyeu,K.D., Laskey,J.G., Riekhof,W.R., VanVickle,S. and Morris,R.O.
AUTHORS A family of cytokinin oxidases from Arabidopsis thaliana
TITLE Unpublished
JOURNAL 2 (bases 1 to 1575)
REFERENCE Bilyeu,K.D., Laskey,J.G., Riekhof,W.R., VanVickle,S. and Morris,R.O.
AUTHORS Direct Submission
TITLE Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall,
JOURNAL Columbia, MO 65211, USA
FEATURES Location/Qualifiers
source 1. .1575
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="V"
1. .1575
/gene="CKX5"
1. .1575
/gene="CKX5"
/codon_start=1
/product="cytokinin oxidase"

gene
CDS

/protein_id="AAG30908.1"
/db_xref="GI:11120514"
/translation="MIAYIEPYFLENDAEAASAATAAGKSTDGVSESLNQGEILCGG
AAADIAGRDFGGMNCVKPLAVRPVGPEDIAGAVKAALRSCLKLTVAAARGNGHSINGQA
MAEGLVDMSTTAENHFVEVGYLSGGDATAFVDVSGGALWEDVLKRCVSEYGLAPRSW
TDYLGTLVGGTLSNAGVSGQAFRYGPQTSNVTELDVVTGNGDVVTCSEIENSELFFSV
LGGLGQFGIITRARVLLQAPADMVRWIRVVYTEFDEFTQDAEWLVSQKNESSEFDYVEG
FVFVNGADPVNGWPTVPLHPDHEFDPTRLPQSCGSVLYCLEGLHYRDSDSNSTIDKR
VERLIGRLRFNEGRFEVDLPYVDFLLRVKRSSEIAKENGWTETPHPWLNLFVSKRDI
GDFNRTVFEKELVKNGVGPMPLVYPLLRSRWDDRTSVVPEEGEIFYIVALLRFVPPCA
KVSSVEKMAVQNOEIVHWCVKNGIDYKLYLPHYKSQEEWIRHFGNWSRFSVDRKAMFD
PMAILSPGQKIFNRSL"

ORIGIN

Alignment Scores:
Pred. No.: 708 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x AF303981 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 502 GTGGGAGGTACGTTGTCAAT 522

RESULT 22
AX653027
LOCUS Oryza sativa 1587 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 2897 from Patent WO03000898.
ACCESSION AX653027
VERSION AX653027.1 GI:29155841
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1
REFERENCE Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
AUTHORS Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 2897 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES Location/Qualifiers
source 1. .1587
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN

Alignment Scores:
Pred. No.: 713 Length: 1587
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX653027 (1-1587)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 523 GTCGGTGGCAGCTCTCCAAC 543

RESULT 23
AX653226
LOCUS Oryza sativa 1590 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3096 from Patent WO03000898.
ACCESSION AX653226
VERSION AX653226.1 GI:29156040

AR150952	LOCUS	AR150952	1605 bp	DNA	linear	PAT 08-AUG-2000
DEFINITION	Sequence 3 from patent US 6229066.					
ACCESSION	AR150952					
VERSION	AR150952.1	GI:15115543				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1605)					
AUTHORS	Morris,R.O.					
TITLE	Cytokinin oxidase					
JOURNAL	Patent: US 6229066-A 3 08-MAY-2001;					
FEATURES	Location/Qualifiers					
source	1..1605					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Alignment Scores:						
Pred. No.:	719	Length:	1605			
Score:	35.00	Matches:	7			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	6	Gaps:	0			
US-10-014-101B-39 (1-7) x AR150952 (1-1605)						
Qy	1 ValGlyGlyThrLeuSerAsn 7					
Db	523 GTCGGCGGCACGCTGTCCAAC 543					
RESULT 26						
AR399211	LOCUS	AR399211	1605 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 3 from patent US 6617497.					
ACCESSION	AR399211					
VERSION	AR399211.1	GI:40137776				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1605)					
AUTHORS	Morris,R.O.					
TITLE	Cytokinin oxidase					
JOURNAL	Patent: US 6617497-A 3 09-SEP-2003;					
FEATURES	Location/Qualifiers					
source	1..1605					
	/organism="unknown"					
	/mol_type="genomic DNA"					
ORIGIN						
Alignment Scores:						
Pred. No.:	719	Length:	1605			
Score:	35.00	Matches:	7			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	6	Gaps:	0			
US-10-014-101B-39 (1-7) x AR399211 (1-1605)						
Qy	1 ValGlyGlyThrLeuSerAsn 7					
Db	523 GTCGGCGGCACGCTGTCCAAC 543					
RESULT 27						
BT002757	LOCUS	BT002757	1606 bp	mRNA	linear	PLN 15-JAN-2003
DEFINITION	Arabidopsis thaliana CKX5 mRNA sequence.					
ACCESSION	BT002757					
VERSION	BT002757.1	GI:27754264				

Oryza sativa	Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M., Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.	Plant genes involved in defense against pathogens	Patent: WO 0300898-A 3096 03-JAN-2003;	Syngenta Participations AG (CH)	Location/Qualifiers	1..1590	/organism="Oryza sativa"	/mol_type="unassigned DNA"	/db_xref="taxon:4530"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														</
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KEYWORDS	FLI CDNA.	TITLE	Regulated expression of genes in plant seeds
SOURCE	Arabidopsis thaliana (thale cress)	JOURNAL	Patent: WO 0063401-A 1 26-OCT-2000;
ORGANISM	Arabidopsis thaliana	PIONEER	HI-BRED INTERNATIONAL, INC. (US)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	FEATURES	Location/Qualifiers
AUTHORS	1 (bases 1 to 1606) Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.	source	1..1608 /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577"
TITLE	Arabidopsis Open Reading Frame (ORF) Clones	CDS	1..1608 /note="unnamed protein product" /codon_start=1 /protein_id="CAC16630.1" /db_xref="GI:11229953" /translation="MAVVYLLLAGLIACSHALAAAGTLALGEDRGPRWPAFLAALALD GKLRTDSNATAAASDFGNITSALPAAVLYPSSSTDGLVALLSAANSTPGWPYTIAFRG RGHSLMGQAFAPGGVVVNMAISLGDAAAAPRVNVSADGRYVDAGGEQVWIDVLRASL ARGVAPRSWTDLYLTVGGTLSNAGISGQAFRHGPQISNVLEMDVITGHGEMVTCSKQ LNADLFDAVLGGLGQFGVITRARIAVEPAPARWRVRLVYTDFAAFSADQERLTAPRP GGGASFGPMSYVEGSVFVNQSLATDLANTGFFTDADVARIVALAGERNATTVYSIEA TLNYDNATAAAAVDQELASVLGTLVYVEGFQFQRDVSYTAFLDVRVHGEVVALNKLGLW RVPHFWLNMVPRSRIDFDRGVFKILQGTDIVGPLIVYPLNKSMDWDDGMSAATPSE DVFYAVSLLFSSVAPNDLARLQEQNRRLRFCDLAGIQYKTYLARHTDRSDWVRHFGA AEWNRFEVMKNKYDPKRLLSPGQDIFN"
JOURNAL	Unpublished	ORIGIN	
REFERENCE	2 (bases 1 to 1606) Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.	Alignment Scores:	
AUTHORS	Direct Submission	Pred. No.:	721 Length: 1608
TITLE	Submitted (15-JAN-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA	Score:	35.00 Matches: 7
JOURNAL	Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.	Percent Similarity:	100.00% Conservative: 0
COMMENT		Best Local Similarity:	100.00% Mismatches: 0
FEATURES	Location/Qualifiers	Query Match:	100.00% Indels: 0
source	1..1606 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /chromosome="4" /clone="C105456" /ecotype="Columbia" /note="This clone is in pUNI 51." 1..1606 /gene="At4g14745" 1..1606 /gene="At4g14745" /gene="At4g14745" /note="This clone does not hit any of the Arabidopsis chromosomes (version July 2002), but it does hit another cDNA entry (Accession Number AF303981 and AY091158) encoding a putative cytokinin oxidase." /evidence=experimental	DB:	6 Gaps: 0
gene		US-10-014-101B-39 (1-7) x AX039923 (1-1608)	
misc_feature		QY 1 ValGlyGlyThrLeuSerAsn 7 Db 529 GTCGGCGGCACGCTGTCCAAC 549	
ORIGIN		RESULT 29 AX339732 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES source	AX339732 Sequence 29 from Patent WO0196580. AX339732 AX339732.1 GI:18135725 Arabidopsis thaliana (thale cress) Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 Schmuelling,T. and Werner,T. Method for modifying plant morphology, biochemistry and physiology Patent: WO 0196580-A 29 20-DEC-2001; Schmuelling, Thomas (DE) ; Werner, Tomas (DE) Location/Qualifiers 1..1611 /organism="Arabidopsis thaliana" /mol_type="unassigned DNA" /db_xref="taxon:3702"
Alignment Scores:		AX339732 Sequence 1 from Patent WO0063401. AX039923 AX039923.1 GI:11229952 Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 Habben,J.E., Zinselmeier,C. and Tomes,D.	1611 bp DNA linear PAT 10-JAN-2002
Pred. No.:	720 Length: 1606		
Score:	35.00 Matches: 7		
Percent Similarity:	100.00% Conservative: 0		
Best Local Similarity:	100.00% Mismatches: 0		
Query Match:	100.00% Indels: 0		
DB:	8 Gaps: 0		
US-10-014-101B-39 (1-7) x BT002757 (1-1606)			
QY 1 ValGlyGlyThrLeuSerAsn 7 Db 502 GTGGGAGGTACGTTGTCAAAT 522			
RESULT 28 AX039923 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	AX039923 Sequence 1 from Patent WO0063401. AX039923 AX039923.1 GI:11229952 Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 Habben,J.E., Zinselmeier,C. and Tomes,D.		
Alignment Scores:			
Pred. No.:	722 Length: 1611		
Score:	35.00 Matches: 7		
Percent Similarity:	100.00% Conservative: 0		
Best Local Similarity:	100.00% Mismatches: 0		
Query Match:	100.00% Indels: 0		
DB:	6 Gaps: 0		
US-10-014-101B-39 (1-7) x AX339732 (1-1611)			

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 499 GTTGGAGGTACACTCTCCAAT 519

RESULT 30
AX785080 1611 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequence 29 from Patent WO03050287.
ACCESSION AX785080
VERSION AX785080.1 GI:32952911
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Schmulling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 03050287-A 29 19-JUN-2003;
Schmulling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES
source Location/Qualifiers
1. .1611
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN
Alignment Scores:
Pred. No.: 722 Length: 1611
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX785080 (1-1611)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 499 GTTGGAGGTACACTCTCCAAT 519

RESULT 31
AX339737 1620 bp DNA linear PAT 10-JAN-2002
LOCUS
DEFINITION Sequence 34 from Patent WO0196580.
ACCESSION AX339737
VERSION AX339737.1 GI:18135729
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Schmulling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 0196580-A 34 20-DEC-2001;
Schmulling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES
source Location/Qualifiers
1. .1620
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN
Alignment Scores:
Pred. No.: 725 Length: 1620
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX339737 (1-1620)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 508 GTTGAGGTACACTCTCCAAT 528

RESULT 32
AX785085 1620 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequence 34 from Patent WO03050287.
ACCESSION AX785085
VERSION AX785085.1 GI:32952915
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Schmulling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 03050287-A 34 19-JUN-2003;
Schmulling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES
source Location/Qualifiers
1. .1620
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN
Alignment Scores:
Pred. No.: 725 Length: 1620
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX785085 (1-1620)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 508 GTTGAGGTACACTCTCCAAT 528

RESULT 33
AF303982 1623 bp mRNA linear PLN 08-NOV-2000
LOCUS
DEFINITION Arabidopsis thaliana cytokinin oxidase (CKX6) mRNA, complete cds.
ACCESSION AF303982
VERSION AF303982.1 GI:11120515
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1623)
AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.
TITLE A family of cytokinin oxidases from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1623)
AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall,
Columbia, MO 65211, USA
FEATURES
source Location/Qualifiers
1. .1623
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"

gene /chromosome="I"
1. .1623
/gene="CKX6"
CDS 1. .1623
/gene="CKX6"
/codon_start=1
/product="cytokinin oxidase"
/protein_id="AAG30909.1"
/db_xref="GI:11120516"
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TVHPSDIASVSSDFGLKSPPEPLAVLHPSSAEDVARLVRTAYGSATAFPVSARGHGH
SINGQAAAGRNGVVMNHGVTGTPKPLVRPDEMYVDVWGELWVDVLKKTLEHGLAP
KSTIDYLYTVGGTLSNAGISGQALHGGPQISNVLELDVVTGKGEVMRCSEEEENTRLF
HGVLGGLGQFGIITRARIISLEPAPQQRVIRVLYSSFKVFTEDQEYLISMHGOLKPDY
VEGFIVDEGLVNNWRSFFSPRPVKISSVSSNGSVLYCLEITKNYHDSSEIVDQE
VEILMKKLNFIPTSVFTTDLQYVDFDRVHKAELKRSKNLMEVPPHPLNLFPKRSRI
SDFDKGVFKGILGNKTSGPILIYPMNKDKWDERSSAVTPDEEVFYLVALLRSLATDGE
ETQKLEYLKDQNNRILEFCEQAKINVKQYLPHPHATQEEWVAHFGDKWDRFRSLKAEFD
PRHILATGQRIQFQNPISLSLFPSSSSSSAAASW"

ORIGIN

Alignment Scores: 726 Length: 1623
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 8

US-10-014-101B-39 (1-7) x AF303982 (1-1623)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
DB 511 GTTGGAGGTACTCTCCAAT 531

RESULT 34

BT000179 Arabidopsis thaliana cytokinin oxidase-like protein (At4g29740)
LOCUS mRNA, complete cds.
DEFINITION BT000179 1655 bp mRNA linear PLN 19-SEP-2002

ACCESSION BT000179 GI:23197941
VERSION BT000179.1 GI:23197941
KEYWORDS FLI CDNA.

SOURCE

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Tripp,M., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (19-SEP-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
e-mail for correspondence: arab@sequence.stanford.edu

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
sequenced the pENTR (ORF) clones using the RAFL cDNAs: Nguyen,M.,
Southwick,A., Tripp,M., Palm,C.J., Jones,T., Wu,T., Chen,H.,
Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toroumi,M.,
Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,

Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

Location/Qualifiers
1. .1655
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
/clone="U16213"
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/note="This clone is in pENTR/SD-dTopo This is a cloned
PCR product using RIKEN clone RAFL07-11-K12 (AY054460) as
a template"
1. .1655
/gene="At4g29740"
/note="synonym: T16L4.250"
1. .1575
/gene="At4g29740"
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/protein_id="AAN15498.1"
/db_xref="GI:23197942"
/translation="MTNTLCLSLITLITLFIISLTPLIKSDEGIDVFLPISLNLTVLT
DPFISAAASHDFGNITDENPGAVLCPSSSTTEVARLLRFANGGFSYNGKSTSPASTFKV
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PKLNPELFYVGLGGLGQFGIITRARIADHAPTRVKWSRILYSDFSFAFKRDQERLISM
TNDLGVDFLEGQLMMSNGFVDTSFPLSDQTRVASLVNDHRIYVLEVAKYDRTTLP
IIDQVIDTLRSLTGFAPGMFVQDVPYDFLNRVNEEDKLSLGLWEVPHPWLNIFV
PGSRIQDFHDGVINGLLLNQTSSTSGVTLYFPTNRKNWNRMSMTWPTDEDVFYVIGLLQ
SAGGSQWQELNLDKVIQFCENSIGIKIKEYLMHYTRKEDWVKHFGPKWDDFLRKKI
MFDPKRLLSPGQDIFN"

gene

CDS

ORIGIN

Alignment Scores: 738 Length: 1655
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x BT000179 (1-1655)

QY 1 ValGlyGlyThrLeuSerAsn 7
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DB 535 GTCGGCGGGACGTTGTCGAAC 555

RESULT 35

AX653630
LOCUS AX653630 1677 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3500 from Patent WO03000898.
ACCESSION AX653630
VERSION AX653630.1 GI:29156444
KEYWORDS

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
Plant genes involved in defense against pathogens
Patent: WO 03000898-A 3500 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES

source

Location/Qualifiers
1. .1677
/organism="Oryza sativa"
/mol_type="unassigned DNA"

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x CQ812635 (1-1728)

QY 1 ValGlyGlyThrLeuSerAsn 7
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Db 574 GTTGGAGGTACACTATCTAAT 594

RESULT 38
AX339728
LOCUS AX339728 1728 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 25 from Patent WO0196580.
ACCESSION AX339728
VERSION AX339728.1 GI:18135721
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Schmullling, T. and Werner, T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 0196580-A 25 20-DEC-2001;
JOURNAL Schmullling, Thomas (DE); Werner, Tomas (DE)
FEATURES Location/Qualifiers
source 1..1728
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 766 Length: 1728
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX339728 (1-1728)

QY 1 ValGlyGlyThrLeuSerAsn 7
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Db 574 GTTGGAGGTACACTATCTAAT 594

RESULT 39
AX785076
LOCUS AX785076 1728 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 25 from Patent WO03050287.
ACCESSION AX785076
VERSION AX785076.1 GI:32952907
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Schmullling, T. and Werner, T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 03050287-A 25 19-JUN-2003;
JOURNAL Schmullling, Thomas (DE); Werner, Tomas (DE)
FEATURES Location/Qualifiers
source 1..1728
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 766 Length: 1728
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x AX785076 (1-1728)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 574 GTTGGAGGTACACTATCTAAT 594

RESULT 40
ZMY18377
LOCUS ZMY18377 1776 bp mRNA linear PLN 10-MAY-1999
DEFINITION Zea mays mRNA for cytokinin oxidase.
ACCESSION Y18377
VERSION Y18377.1 GI:3882017
KEYWORDS cytokinin oxidase.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE Houba-Herlin, N., Pethe, C., d'Alayer, J. and Laloue, M.
AUTHORS Cytokinin oxidase from Zea mays: purification, cDNA cloning and
TITLE expression in moss protoplasts
JOURNAL Plant J. 17 (6), 615-626 (1999)
MEDLINE 99246676
PUBMED 10230061
REFERENCE 2 (bases 1 to 1776)
AUTHORS Laloue, M.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1998) M. Laloue, INRA Laboratoire de Biologie
Cellulaire, Route de Saint-Cyr, F-78026 Versailles Cedex, FRANCE
COMMENT Conflicting sequence: AF044603.
FEATURES Location/Qualifiers
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38..1642
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/db_xref="UniProt/Swiss-Prot:Q9TON8"
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GVAPRSWTDYLYLTVGGLSNAGISGQAFRHGPOISNVLEMDVITGHGEMVTCCKQLN
ADLFDVGLGLGQFGVITRAIAPAPARARWRVLTDFAAFSADQERLTAPRPGG
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ORIGIN

Alignment Scores:
Pred. No.: 783 Length: 1776
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x ZMY18377 (1-1776)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 560 GTCGGCGGCACGCTGTCCAAC 580

Search completed: February 18, 2005, 05:21:31
Job time : 963.84 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2005, 21:47:40 ; Search time 125.02 Seconds
(without alignments)
331.452 Million cell updates/sec

Title: US-10-014-101B-39
Perfect score: 35
Sequence: 1 VGGTSLN 7

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:
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2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002as:
7: Geneseqn2002bs:
8: Geneseqn2003as:
9: Geneseqn2003bs:
10: Geneseqn2003cs:
11: Geneseqn2003ds:
12: Geneseqn2004as:
13: Geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	342	8 ABZ56423	Abz56423 Aspergill
2	35	100.0	442	3 AAC02606	Aac02606 Human sec
3	35	100.0	566	10 ADH61273	Adh61273 Soybean c
4	35	100.0	579	13 ACN59295	Acn59295 Cotton gy
5	35	100.0	641	13 ACN54124	Acn54124 Cotton an

6	35	100.0	1506	6 ABK28625	Abk28625 cDNA enco
7	35	100.0	1506	9 ACC85294	Acc85294 Arabidops
8	35	100.0	1506	12 ADO06498	Ado06498 A thalian
9	35	100.0	1515	6 ABK28629	Abk28629 cDNA enco
10	35	100.0	1515	9 ACC85298	Acc85298 Arabidops
11	35	100.0	1548	3 AAC43214	Aac43214 Arabidops
12	35	100.0	1566	8 ADA71115	Ada71115 Rice gene
13	35	100.0	1572	6 ABK28626	Abk28626 cDNA enco
14	35	100.0	1572	9 ACC85295	Acc85295 Arabidops
15	35	100.0	1572	10 ADH61268	Adh61268 Arabidops
16	35	100.0	1575	3 AAC42983	Aac42983 Arabidops
17	35	100.0	1575	6 ABZ14284	Abz14284 Arabidops
18	35	100.0	1575	6 ABK28627	Abk28627 cDNA enco
19	35	100.0	1575	8 ADA68648	Ada68648 Arabidops
20	35	100.0	1575	9 ACC85296	Acc85296 Arabidops
21	35	100.0	1575	10 ADH61269	Adh61269 Arabidops
22	35	100.0	1575	10 ADH61270	Adh61270 Arabidops
23	35	100.0	1587	8 ADA69574	Ada69574 Rice gene
24	35	100.0	1590	8 ADA69773	Ada69773 Rice gene
25	35	100.0	1593	8 ADA69430	Ada69430 Rice gene
26	35	100.0	1605	2 AAX02914	Aax02914 Z. mays c
27	35	100.0	1608	3 AAC86501	Aac86501 DNA encod
28	35	100.0	1611	6 ABK28628	Abk28628 cDNA enco
29	35	100.0	1611	9 ACC85297	Acc85297 Arabidops
30	35	100.0	1620	6 ABK28632	Abk28632 cDNA enco
31	35	100.0	1620	9 ACC85301	Acc85301 Arabidops
32	35	100.0	1623	10 ADH61271	Adh61271 Arabidops
33	35	100.0	1655	10 ADH61279	Adh61279 Arabidops
34	35	100.0	1677	8 ADA70177	Ada70177 Rice gene
35	35	100.0	1719	13 ADS49453	Ads49453 Bacterial
36	35	100.0	1728	6 ABK28624	Abk28624 cDNA enco
37	35	100.0	1728	9 ACC85293	Acc85293 Arabidops
38	35	100.0	1728	12 ADO06496	Ado06496 A thalian
39	35	100.0	1857	10 ADH61281	Adh61281 Barley cy
40	35	100.0	1873	10 ADH61280	Adh61280 Arabidops
41	35	100.0	1936	6 ABK28611	Abk28611 DNA encod
42	35	100.0	1936	9 ACC85280	Acc85280 Arabidops
43	35	100.0	2236	6 ABK28606	Abk28606 DNA encod
44	35	100.0	2236	9 ACC85275	Acc85275 Arabidops
45	35	100.0	2282	12 ADP03325	Adp03325 Rice grai

ALIGNMENTS

RESULT 1	
ABZ56423	
ID	ABZ56423 standard; cDNA; 342 BP.
XX	
AC	ABZ56423;
XX	
DT	28-MAR-2003 (first entry)
XX	
DE	Aspergillus oryzae polynucleotide SEQ ID NO 5536.
XX	
KW	Aspergillus oryzae; fermentation; fungus; industrial; EST;
KW	expressed sequence tag; gene; ss.
OS	Aspergillus oryzae.
XX	
PN	WO200279476-A1.
XX	
PD	10-OCT-2002.
XX	
PF	22-MAR-2002; 2002WO-IB000890.
XX	
PR	30-MAR-2001; 2001JP-00098371.
XX	
PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA	(NARE-) NAT RES INST BREWING.
PA	(NORQ) NAT FOOD RES INST MIN AGRIC.
XX	
PI	Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
PI	Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;

XX WPI; 2003-046917/04.

XX Detection of expression of specific *Aspergillus* genes for monitoring the

PT fermentation and growth conditions of the fungus, using DNA probes.

PT

XX Claim 1; SEQ ID NO 5536; 48pp + Sequence Listing; Japanese.

XX

CC The invention relates to a polynucleotide having any of 6006 specific

CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under

CC specific culture conditions including one or more of eutrophic,

CC oligotrophic, solid, early germination, alkaline, high temperature, low

CC temperature or maltose culture or polynucleotides stringently hybridising

CC to these sequences. The polynucleotides are useful for monitoring the

CC progress of fermentation and the growth conditions of a fungus,

CC especially of *Aspergillus oryzae* which is widely used in industrial

CC fermentation. Also monitoring for fungal contamination. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 342 BP; 97 A; 79 C; 88 G; 78 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	99.5	Length:	342
Score:	35.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-014-101B-39 (1-7) x ABZ56423 (1-342)

QY 1 ValGlyGlyThrLeuSerAsn 7

Db 85 GTTGAGGGACACTGAGCAAT 105

RESULT 2

AAC02606/c

ID AAC02606 standard; cDNA; 442 BP.

XX

AC AAC02606;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST, SEQ ID NO: 2604.

XX

XW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.

XX

OS Homo sapiens.

XX

PN EP1033401-A2.

XX

PD 06-SEP-2000.

XX

PF 21-FEB-2000; 2000EP-00200610.

XX

PR 26-FEB-1999; 99US-0122487P.

XX

PA (GEST) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX

XX WPI; 2000-500381/45.

DR P-PSDB; AAG02600.

XX

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX

PS Claim 1; SEQ ID NO 2604; 71pp + Sequence Listing; English.

XX

CC The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. An ORF has been identified within the

CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs

CC derived from 30 different tissues. EST sequences usually correspond

CC mainly to the 3' untranslated region (UTR) of the mRNA because they are

CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not

CC well suited for isolating cDNA sequences derived from the 5' ends of

CC mRNAs and even in those cases where longer cDNA sequences have been

CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from

CC mRNAs with intact 5' ends and can therefore be used to obtain full length

CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,

CC gene therapy and chromosome mapping procedures. They are used to obtain

CC upstream regulatory sequences and to design expression and secretion

CC vectors

XX

SQ Sequence 442 BP; 154 A; 76 C; 116 G; 95 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	132	Length:	442
Score:	35.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-014-101B-39 (1-7) x AAC02606 (1-442)

QY 1 ValGlyGlyThrLeuSerAsn 7

Db 67 GTGGCGGGAACGCTTCTAAT 47

RESULT 3

ADH61273

ID ADH61273 standard; DNA; 566 BP.

XX

AC ADH61273;

XX

DT 25-MAR-2004 (first entry)

XX

DE Soybean cytokinin oxidase (CKX1) DNA #2.

XX

KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;

KW CKX1; soybean; ds; gene.

XX

OS Glycine max.

XX

PN US2003163847-A1.

XX

PD 28-AUG-2003.

XX

PF 20-DEC-2002; 2002US-00326184.

XX

PR 20-DEC-2001; 2001US-0343129P.

XX

PA (PHAA) PHARMACIA CORP.

XX

PI Huang S, Crossland LD, Cheikh N, Morris RO;

XX

DR WPI; 2003-897983/82.

DR GENBANK; BU084470.

XX

PT Producing plants characterized by reversible male-sterility, useful for

PT maintaining male sterility in plants, by transforming a plant cell with a

PT nucleic acid construct containing a polynucleotide encoding a cytokinin

PT oxidase.

XX

PS Disclosure; SEQ ID NO 14; 33pp; English.

XX

XX The invention relates to a method for producing a plant characterised by

CC reversible male-sterility which involves transforming a plant cell with a

CC nucleic acid construct containing a polynucleotide encoding a cytokinin

CC oxidase. The method is useful for producing reversible male-sterility in

CC transgenic plants, or for maintaining male sterility in plants. The

CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is soybean cytochrome oxidase (CKX1) DNA. This sequence is used
CC to illustrate the method of the invention.

SQ Sequence 566 BP; 162 A; 115 C; 132 G; 157 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 174 Length: 566
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-39 (1-7) x ADH61273 (1-566)

QY 1 ValGlyGlyThrLeuSerAsn 7

DB 133 GTGGGAGGACACTTCCAT 153

RESULT 4

ACN59295
ID ACN59295 standard; cDNA; 579 BP.

XX ACN59295;

XX 02-DEC-2004 (first entry)

XX Cotton gynoecium tissue EST Clone ID: LIB3829-029-Q6-K6-G4, SEQ:14076.

XX Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium;
KW variety Nucotton33B; library LIB3829; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.

XX Gossypium hirsutum.

XX US2004123340-A1.

XX 24-JUN-2004.

XX 12-DEC-2001; 2001US-00021323.

XX 14-DEC-2000; 2000US-0255619P.

XX (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;

XX WPI; 2004-479808/45.

XX New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
PT tags to map genes.

XX Claim 1; SEQ ID NO 14076; 34pp; English.

XX The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucotton33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct

CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determine whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a
CC cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the US
CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340

XX SQ Sequence 579 BP; 130 A; 136 C; 173 G; 138 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.: 178 Length: 579
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-39 (1-7) x ACN59295 (1-579)

QY 1 ValGlyGlyThrLeuSerAsn 7

DB 209 GTTGTGGACCTTGCTAAC 229

RESULT 5

ACN54124

ID ACN54124 standard; cDNA; 641 BP.

XX ACN54124;

XX 02-DEC-2004 (first entry)

XX Cotton androecium tissue EST Clone ID: LIB3828-021-Q1-K6-C8, SEQ:8905.

XX Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
KW variety Nucotton33B; library LIB3828; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.

XX Gossypium hirsutum.

XX US2004123340-A1.

XX 24-JUN-2004.

XX 12-DEC-2001; 2001US-00021323.

XX 14-DEC-2000; 2000US-0255619P.

XX (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;

XX WPI; 2004-479808/45.

PT New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
XX tags to map genes.
PS Claim 1; SEQ ID NO 8905; 34pp; English.
XX
XX The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeceum
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucotton33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determining whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a
CC cotton variety Nucotton33B androecium tissue cDNA library (LIB3828). The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the US
CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
XX
SQ Sequence 641 BP; 147 A; 156 C; 172 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 200 Length: 641
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-39 (1-7) x ACN54124 (1-641)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 541 GTTGGTGGAACTTGCTAAC 561

RESULT 6
ABK28625

ID ABK28625 standard; cDNA; 1506 BP.

XX ABK28625;

XX 09-APR-2002 (first entry)

XX cDNA encoding A. thaliana cytokinin oxidase AtCKX2.

XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX Arabidopsis thaliana.

XX WO200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-EP006833.
PF 16-JUN-2000; 2000EP-00870132.
XX 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX

PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.

XX Schmulling T, Werner T;

XX WPI; 2002-130736/17.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.

PS Claim 2; Page 146-147; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention

SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 516 Length: 1506
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x ABK28625 (1-1506)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 466 GTCGGAGGACGTTGTCGAAT 486

RESULT 7

ACC85294

ID ACC85294 standard; cDNA; 1506 BP.

XX ACC85294;

XX 18-SEP-2003 (first entry)

XX Arabidopsis cytokinin oxidase-like protein 2 cDNA.

XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

XX Arabidopsis thaliana.

XX WO2003050287-A2.

PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2003-541577/51.
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 167-168; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 516 Length: 1506
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-39 (1-7) x ACC85294 (1-1506)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGAGGAGACGTTGTGCGAAT 486
RESULT 8
ADO06498
ID ADO06498 standard; DNA; 1506 BP.
XX
AC ADO06498;
XX
DT 29-JUL-2004 (first entry)
XX
DE A thaliana cytokinin oxidase AtCKX2 coding sequence.
XX
KW bioremediation; AtCKX2; cytokinin availability; contaminant;
KW metal deficiency; nutrition; ds; gene; cytokinin oxidase.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 1..1506
FT /*tag= a
FT /product= "AtCKX2"
XX
PN WO2004038027-A1.
XX
PD 06-MAY-2004.

XX 24-OCT-2003; 2003WO-EP012051.
PF
XX 24-OCT-2002; 2002EP-00079481.
PR
XX (CROP-) CROPDESIGN NV.
PA
XX Van Camp W;
PI
XX WPI; 2004-375913/35.
DR P-PSDB; ADO06499.
XX
PT Method for bioremediation, useful for removing contaminants or metals, by
PT decreasing cytokinin availability in plants, and cultivating plant on
PT substrate comprising one or more contaminants.
XX
PS Claim 8; Page 55; 61pp; English.
XX
CC The present invention relates to a method for bioremediation, which
CC involves decreasing cytokinin availability in a plant relative to a
CC corresponding wild type plant, and cultivating the plant on a substrate
CC comprising one or more contaminants, or cultivating a plant having
CC lowered availability of cytokinin relative to corresponding wild type
CC plants, on a substrate, which is to be treated. The method is useful for
CC bioremediation, for concentration of contaminants in a plant, where the
CC plant has a higher concentration of contaminants compared to a
CC corresponding wild type plant. The metal contaminants include aluminum,
CC americium, antimony, arsenic, barium, beryllium, bismuth, cadmium,
CC caesium, cerium, chromium, copper, gallium, germanium, gold, indium,
CC iridium, iron, lead, manganese, mercury, molybdenum, neptunium, osmium,
CC palladium, platinum, plutonium, radium, rhenium, rhodium, rubidium,
CC ruthenium, scandium, selenium, silver, strontium, technetium, tellurium,
CC thallium, tin, tungsten, uranium, vanadium or yttrium, preferably
CC cadmium. The plant obtained by the method is useful in bioremediation.
CC Transgenic plants with a lower availability of cytokinin are useful in
CC the manufacture of a medicament for treatment of disorders arising from
CC metal deficiencies, and as a medicament for improving animal or human
CC nutrition. The present sequence is a coding sequence shown in the
CC exemplification of the invention.
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 516 Length: 1506
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-014-101B-39 (1-7) x ADO06498 (1-1506)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGAGGAGACGTTGTGCGAAT 486
RESULT 9
ABK28629
ID ABK28629 standard; cDNA; 1515 BP.
XX
AC ABK28629;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX6.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.

XX PD 20-DEC-2001.
XX PF 18-JUN-2001; 2001WO-EP006833.
XX PR 16-JUN-2000; 2000EP-00870132.
XX PR 27-DEC-2000; 2000US-0258415P.
XX PR 16-MAR-2001; 2001EP-00870053.
XX (SCHM/) SCHMULLING T.
XX PA (WERN/) WERNER T.
XX PI Schmullling T, Werner T;
XX DR WPI; 2002-130736/17.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Example 1; Page 149; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarpy; improving standability of the seedlings;
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1515 BP; 456 A; 327 C; 378 G; 354 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 519 Length: 1515
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-39 (1-7) x ABK28629 (1-1515)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 493 GTAGGTGGTACTCTGTCCAAT 513
RESULT 10
ACC85298
ID ACC85298 standard; cDNA; 1515 BP.
XX
AC ACC85298;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 6 cDNA.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX

PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
XX (SCHM/) SCHMULLING T.
XX PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2003-541577/51.
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 2; Page 171-172; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1515 BP; 456 A; 327 C; 378 G; 354 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 519 Length: 1515
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-39 (1-7) x ACC85298 (1-1515)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 493 GTAGGTGGTACTCTGTCCAAT 513
RESULT 11
AAC43214
ID AAC43214 standard; DNA; 1548 BP.
XX
AC AAC43214;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.

XX		
PR	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130891P.
PR	28-APR-1999;	99US-0131449P.
PR	30-APR-1999;	99US-0132048P.
PR	30-APR-1999;	99US-0132407P.
PR	04-MAY-1999;	99US-0132484P.
PR	05-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	06-MAY-1999;	99US-0132487P.
PR	07-MAY-1999;	99US-0132863P.
PR	11-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134221P.
PR	14-MAY-1999;	99US-0134370P.
PR	18-MAY-1999;	99US-0134768P.
PR	19-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	10-JUN-1999;	99US-0138847P.
PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.
PR	16-JUN-1999;	99US-0139453P.
PR	17-JUN-1999;	99US-0139492P.
PR	18-JUN-1999;	99US-0139454P.
PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139456P.
PR	18-JUN-1999;	99US-0139457P.
PR	18-JUN-1999;	99US-0139458P.
PR	18-JUN-1999;	99US-0139459P.
PR	18-JUN-1999;	99US-0139460P.
PR	18-JUN-1999;	99US-0139461P.
PR	18-JUN-1999;	99US-0139462P.
PR	18-JUN-1999;	99US-0139463P.
PR	18-JUN-1999;	99US-0139750P.
PR	18-JUN-1999;	99US-0139763P.
PR	21-JUN-1999;	99US-0139817P.
PR	22-JUN-1999;	99US-0139899P.
PR	23-JUN-1999;	99US-0140353P.
PR	23-JUN-1999;	99US-0140354P.
PR	24-JUN-1999;	99US-0140695P.
PR	28-JUN-1999;	99US-0140823P.
PR	29-JUN-1999;	99US-0140991P.
PR	30-JUN-1999;	99US-0141287P.
PR	01-JUL-1999;	99US-0141842P.
PR	01-JUL-1999;	99US-0142154P.
PR	02-JUL-1999;	99US-0142055P.
PR	06-JUL-1999;	99US-0142390P.
PR	08-JUL-1999;	99US-0142803P.
PR	09-JUL-1999;	99US-0142920P.
PR	12-JUL-1999;	99US-0142977P.
PR	13-JUL-1999;	99US-0143542P.
PR	14-JUL-1999;	99US-0143624P.
PR	15-JUL-1999;	99US-0144005P.
PR	16-JUL-1999;	99US-0144085P.
PR	16-JUL-1999;	99US-0144086P.
PR	19-JUL-1999;	99US-0144325P.
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PR	20-JUL-1999;	99US-0144632P.
PR	20-JUL-1999;	99US-0144884P.
PR	21-JUL-1999;	99US-0144814P.
PR	21-JUL-1999;	99US-0145086P.
PR	21-JUL-1999;	99US-0145088P.
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PR	22-JUL-1999;	99US-0145089P.
PR	22-JUL-1999;	99US-0145192P.
PR	23-JUL-1999;	99US-0145145P.
PR	23-JUL-1999;	99US-0145218P.
PR	23-JUL-1999;	99US-0145224P.
PR	26-JUL-1999;	99US-0145276P.
PR	27-JUL-1999;	99US-0145913P.
PR	27-JUL-1999;	99US-0145918P.
PR	27-JUL-1999;	99US-0145919P.
PR	28-JUL-1999;	99US-0145951P.
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PR	02-AUG-1999;	99US-0146388P.
PR	02-AUG-1999;	99US-0146389P.
PR	03-AUG-1999;	99US-0147038P.
PR	04-AUG-1999;	99US-0147204P.
PR	04-AUG-1999;	99US-0147302P.
PR	05-AUG-1999;	99US-0147192P.
PR	05-AUG-1999;	99US-0147260P.
PR	06-AUG-1999;	99US-0147303P.
PR	06-AUG-1999;	99US-0147416P.
PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
PR	10-AUG-1999;	99US-0148171P.
PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
PR	16-AUG-1999;	99US-0149368P.
PR	17-AUG-1999;	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.
PR	20-AUG-1999;	99US-0149723P.
PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149902P.
PR	23-AUG-1999;	99US-0149930P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
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PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.

PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 532 Length: 1548
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-39 (1-7) x AAC43214 (1-1548)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGAGGAGACGTTGTGCAAT 486

RESULT 12
ADA71115
ID ADA71115 standard; DNA; 1566 BP.
XX
AC ADA71115;
XX 20-NOV-2003 (first entry)
DT
XX Rice gene, SEQ ID 4438.
DE
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
XX WO2003000898-A1.
FN
XX 03-JAN-2003.
PD
XX 22-JUN-2001; 2001WO-IB001105.
PF
XX 22-JUN-2001; 2001WO-IB001105.
PR
XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
DR
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 4438; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1566 BP; 422 A; 391 C; 371 G; 382 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 539 Length: 1566
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x ADA71115 (1-1566)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 499 GTTGAGGCACACTGTGCAAT 519

RESULT 13
ABK28626

ID ABK28626 standard; cDNA; 1572 BP.

XX
AC ABK28626;

DT 09-APR-2002 (first entry)

DE cDNA encoding A. thaliana cytokinin oxidase AtCKX3.

XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.

OS Arabidopsis thaliana.

XX WO200196580-A2.

XX 20-DEC-2001.

PF 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

PR 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2002-130736/17.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 3; Page 147; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell: (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC inducing leaf thickness; reducing or increasing the vessel size;
CC increasing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;

Alignment Scores: 541 Length: 1572
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-014-101B-39 (1-7) x ABK28626 (1-1572)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTCGGTGGGACGTTATCAAAC 537

RESULT 14

ACC85295
ID ACC85295 standard; cDNA; 1572 BP.
XX
AC ACC85295;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 3 cDNA.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX WPI; 2003-541577/51.
XX

PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 168-169; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;

Alignment Scores: 541 Length: 1572
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 9

US-10-014-101B-39 (1-7) x ACC85295 (1-1572)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTCGGTGGGACGTTATCAAAC 537

RESULT 15

ADH61268
ID ADH61268 standard; DNA; 1572 BP.
XX
AC ADH61268;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #2.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.
XX
PR 20-DEC-2001; 2001US-0343129P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX WPI; 2003-897983/82.
DR GENBANK; AF303979.
XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Claim 42; SEQ ID NO 9; 33pp; English.

XX The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.

SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;

Alignment Scores: 541 Length: 1572
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 10

US-10-014-101B-39 (1-7) x ADH61268 (1-1572)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 517 GTCGGTGGGACGTTATCAAAAC 537

RESULT 16

AAC42983

ID AAC42983 standard; DNA; 1575 BP.

XX AAC42983;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37588.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 05-MAY-1999; 99US-0132484P.

PR 06-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 27-MAY-1999; 99US-0136392P.
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PR 01-JUN-1999; 99US-0137222P.
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PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
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PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
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PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
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PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
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PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 27-JUL-1999; 99US-0145951P.
PR 28-JUL-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
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PR 13-AUG-1999; 99US-0148565P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores: 542 Length: 1575
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 3

US-10-014-101B-39 (1-7) x AAC42983 (1-1575)

Oy 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGCGGGACGTTGTCGAAC 555

RESULT 17
ABZ14284
ID ABZ14284 standard; DNA; 1575 BP.
XX
AC ABZ14284;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2089.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 2089; 577pp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)
detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 542 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x ABZ14284 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 535 GTCGGCGGGACGTTGTCGAAC 555

RESULT 18
ABK28627
ID ABK28627 standard; cDNA; 1575 BP.
XX
AC ABK28627;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX4.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2002-130736/17.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 147-148; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarpy; improving standability of the seedlings;

CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 542 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x ABK28627 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 535 GTCGGCGGGACGTTGTCGAAC 555

RESULT 19
ADA68648
ID ADA68648 standard; DNA; 1575 BP.
XX
AC ADA68648;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 428.
XX
KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 428; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 542 Length: 1575

Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x ADA68648 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTGCAAC 555

RESULT 20

ACC85296

ID ACC85296 standard; cDNA; 1575 BP.

XX

AC ACC85296;

XX 18-SEP-2003 (first entry)

XX Arabidopsis cytokinin oxidase-like protein 4 cDNA.

DE Maize; root growth; root geotropism; cytokinin oxidase; seed size;

XX embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

KW Arabidopsis thaliana.

XX WO2003050287-A2.

PN 19-JUN-2003.

PD 10-DEC-2002; 2002WO-EP013990.

XX 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

PI WPI; 2003-541577/51.

XX Stimulating root growth, enhancing lateral or adventitious root formation

PT or altering root geotropism comprises increasing plant cytokinin oxidase

PT levels or other protein or nucleic acid that reduces active cytokinins in

PT a plant.

XX Claim 2; Page 169-170; 177pp; English.

PS The present invention relates to a method for stimulating root growth or

XX enhancing the formation of lateral or adventitious roots or altering root

CC geotropism, which comprises increasing in a plant or plant part the level

CC of a plant cytokinin oxidase or other protein that reduces the level of

CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and

CC coding sequences from Arabidopsis thaliana are also provided. The method

CC is useful in modifying plant morphological, biochemical and physiological

CC properties, such as in modifying the initiation, stimulation or

CC enhancement of root growth, adventitious root formation, lateral root

CC formation, root geotropism, shoot growth, apical dominance, branching,

CC timing of senescence, timing of flowering, flower formation, seed

CC development and/or seed yield. The present sequence is a coding sequence

CC shown in the invention

XX Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 542 Length: 1575

Score: 35.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x ACC85296 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTGCAAC 555

RESULT 21

ADH61269

ID ADH61269 standard; DNA; 1575 BP.

XX ADH61269;

XX 25-MAR-2004 (first entry)

XX Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #3.

DE Male-sterility; cytokinin oxidase; transgenic plant; seed production;

XX CKX1; mouse-ear cress; gene; ds.

KW Arabidopsis thaliana.

XX US2003163847-A1.

XX 28-AUG-2003.

XX 20-DEC-2002; 2002US-00326184.

XX 20-DEC-2001; 2001US-0343129P.

XX (PHAA) PHARMACIA CORP.

XX Huang S, Crossland LD, Cheikh N, Morris RO;

PI WPI; 2003-897983/82.

XX GENBANK; AF303980.

XX Producing plants characterized by reversible male-sterility, useful for

PT maintaining male sterility in plants, by transforming a plant cell with a

PT nucleic acid construct containing a polynucleotide encoding a cytokinin

PT oxidase.

XX Claim 43; SEQ ID NO 10; 33pp; English.

PS The invention relates to a method for producing a plant characterised by

XX reversible male-sterility which involves transforming a plant cell with a

CC nucleic acid construct containing a polynucleotide encoding a cytokinin

CC oxidase. The method is useful for producing reversible male-sterility in

CC transgenic plants, or for maintaining male sterility in plants. The

CC method reduces the expense of seed production for existing hybrid plants

CC such as corn, but also makes it possible to produce hybrid varieties of

CC traditionally non-hybrid crops. The method is also useful for introducing

CC economically valuable traits from plants having undesirable production

CC characteristics into plants having desirable characteristics. The present

CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This

CC sequence is used to illustrate the method of the invention.

XX Sequence 1575 BP; 418 A; 367 C; 349 G; 441 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 542 Length: 1575

Score: 35.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-10-014-101B-39 (1-7) x ADH61269 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTGCAAC 555

RESULT 22

ADH61270
ID ADH61270 standard; DNA; 1575 BP.
XX AC ADH61270;
XX DT 25-MAR-2004 (first entry)
XX DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #4.
XX KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
XX KW CKX1; mouse-ear cress; gene; ds.
XX OS Arabidopsis thaliana.
XX PN US2003163847-A1.
XX PD 28-AUG-2003.
XX PF 20-DEC-2002; 2002US-00326184.
XX PR 20-DEC-2001; 2001US-0343129P.
XX PA (PHAA) PHARMACIA CORP.
XX PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX WPI; 2003-897983/82.
XX DR GENBANK; AF303981.
XX PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX PS Claim 44; SEQ ID NO 11; 33pp; English.
XX CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.
XX SQ Sequence 1575 BP; 390 A; 328 C; 451 G; 406 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 542 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-014-101B-39 (1-7) x ADH61270 (1-1575)
Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 502 GTGGAGGTACGTTGTCAAT 522
RESULT 23
ADA69574
ID ADA69574 standard; DNA; 1587 BP.
XX AC ADA69574;
XX DT 20-NOV-2003 (first entry)
XX XX

DE Rice gene, SEQ ID 2897.
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX OS Oryza sativa.
XX PN WO2003000898-A1.
XX PD 03-JAN-2003.
XX PF 22-JUN-2001; 2001WO-IB001105.
XX PR 22-JUN-2001; 2001WO-IB001105.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX DR Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
XX PS Claim 6; SEQ ID NO 2897; 899pp; English.
XX CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX SQ Sequence 1587 BP; 307 A; 462 C; 458 G; 356 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 547 Length: 1587
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-014-101B-39 (1-7) x ADA69574 (1-1587)
Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 523 GTCGGTGGCAGGCTCTCCAAC 543
RESULT 24
ADA69773
ID ADA69773 standard; DNA; 1590 BP.
XX AC ADA69773;
XX DT 20-NOV-2003 (first entry)
XX DE Rice gene, SEQ ID 3096.
XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX KW gene; ds.
XX OS Oryza sativa.
XX PN WO2003000898-A1.
XX XX

PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 3096; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1590 BP; 356 A; 465 C; 460 G; 309 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 548 Length: 1590
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x ADA69773 (1-1590)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 520 GTCGGTGGCACCTTGTCGAAT 540

RESULT 25
ADA69430
ID ADA69430 standard; DNA; 1593 BP.
XX
AC ADA69430;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 2753.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
XX WO2003000898-A1.
PN
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI

PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 2753; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 1593 BP; 232 A; 523 C; 569 G; 269 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 549 Length: 1593
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x ADA69430 (1-1593)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTGGGGCGCACCTCTCCAAC 537

RESULT 26
AAX02914
ID AAX02914 standard; DNA; 1605 BP.
XX
AC AAX02914;
XX
DT 20-MAY-1999 (first entry)
XX
DE Z. mays cks1 DNA coding region.
XX
KW Cytokinin oxidase; cks1; transgenic plant; altered growth behaviour;
KW cytokinin-associated pathogenesis; resistance; fungi; nematode; assay;
KW grain yield; secondary growth; metabolism; senescence; ss.
XX
OS Zea mays.
XX
PN WO9906571-A1.
XX
PD 11-FEB-1999.
XX
PF 30-JUL-1998; 98WO-US015844.
XX
PR 30-JUL-1997; 97US-0054268P.
PR 29-JUL-1998; 98US-00124541.
XX
PA (UMOR) UNIV MISSOURI.
XX
PI Morris RO;
XX
DR WPI; 1999-153800/13.
DR P-PSDB; AAW93007.
XX
PT New cytokinin oxidase from maize - used to generate transgenic plants
PT with, e.g. better disease resistance and growth characteristics.
XX

PS Claim 7b; Page 64-69; 140pp; English.

XX This sequence encodes a Zea mays cytokinin oxidase, cklx1. This gene is used to generate transgenic plants in which cytokinin-associated pathogenesis or growth behaviour is altered. Particularly applications include generation of plants with increased resistance to fungi and nematodes, increased grain yield and superior secondary growth properties. Host cells are used for production of recombinant cklx1 nucleic acid which is useful in an assay for determining cytokinin concentrations, and for its studying effects on plant growth and metabolism, including senescence

SQ Sequence 1605 BP; 236 A; 560 C; 561 G; 248 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	553	Length:	1605
Score:	35.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-014-101B-39 (1-7) x AAX02914 (1-1605)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 523 GTCGGCGGCACGCTGTCCAAC 543

RESULT 27

AAC86501

ID AAC86501 standard; DNA; 1608 BP.

XX

AC AAC86501;

XX

DT 19-MAR-2001 (first entry)

XX

DE DNA encoding a maize cytokinin oxidase polypeptide.

XX

KW Cytokinin oxidase; temporal gene expression; spatial gene expression; plant seed; cytokinin modulating gene; transgenic plant; seed size; stress tolerance; yield stability; tip kernel abortion; seed set; ss.

XX

OS Zea mays.

XX

FH Key

FT CDS

FT Location/Qualifiers

FT 1. .1608

FT /*tag= a

FT /product= "cytokinin oxidase"

XX

FN WO2000063401-A1.

XX

PD 26-OCT-2000.

XX

PF 13-APR-2000; 2000WO-US009943.

XX

PR 16-APR-1999; 99US-0129844P.

XX

PA (PION-) PIONEER HI-BRED INT INC.

XX

PI Habben JE, Zinselmeier C, Tomes D;

XX

DR WPI; 2000-672743/65.

DR P-PSDB; AAB30691.

XX

PT Novel recombinant DNA construct useful for producing transgenic plants having enhanced levels of cytokinin expression, improved stress tolerance and yield stability.

PT

XX Disclosure; Page 63-65; 76pp; English.

PS

XX The present sequence encodes a maize cytokinin oxidase polypeptide. It is used to produce the recombinant DNA molecules of the invention. These comprise a genetic construct consisting of a promoter directing temporal

CC and/or spatial gene expression in plant seed operatively linked to a cytokinin modulating gene. The recombinant DNA molecules are useful for producing fertile, transgenic plants capable of regulated expression of a cytokinin modulating gene in developing seeds. They are also useful for improving stress tolerance and yield stability in plants. The preferential expression of recombinant DNA molecules of the invention occurs about 14-25 days after pollination. The transgenic plants thus produced have enhanced levels of cytokinin expression exhibit improved seed size, decreased tip kernel abortion and increased seed set during unfavourable environmental conditions

XX

SQ Sequence 1608 BP; 237 A; 561 C; 560 G; 250 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	555	Length:	1608
Score:	35.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-014-101B-39 (1-7) x AAC86501 (1-1608)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 529 GTCGGCGGCACGCTGTCCAAC 549

RESULT 28

ABK28628

ID ABK28628 standard; cDNA; 1611 BP.

XX

AC ABK28628;

XX

DT 09-APR-2002 (first entry)

XX

DE cDNA encoding A. thaliana cytokinin oxidase AtCKX5.

XX

KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant; root growth; lateral root; adventitious root; root geotropism; herbicide; root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX

OS Arabidopsis thaliana.

XX

PN WO200196580-A2.

XX

PD 20-DEC-2001.

XX

PF 18-JUN-2001; 2001WO-EP006833.

XX

PR 16-JUN-2000; 2000EP-00870132.

PR 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.

XX

PA (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX

PI Schmullling T, Werner T;

XX

DR WPI; 2002-130736/17.

XX

PT Polynucleotide encoding novel plant protein having cytokinin oxidase activity and the protein useful for stimulating root growth, enhancing the formation of lateral or adventitious roots, altering root geotropism.

PT

XX Claim 3; Page 148-149; 154pp; English.

PS

XX The invention relates to an isolated polynucleotide (I) encoding a novel plant protein (II) having cytokinin oxidase activity. (I) is useful for production of transgenic plants, plant cells or tissues; for production of altered plants, plant cell or tissues; and for effecting the expression of (II) where (I) is operably linked to one or more control sequences. The methods further comprises regenerating a plant from the plant cell. (I) and (II) are useful for stimulating root growth;

CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;

Alignment Scores: 556 Length: 1611
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-014-101B-39 (1-7) x ABK28628 (1-1611)

QY 1 ValGlyGlyThrLeuSerAsn 7
DB 499 GTTGAGGTACACTCTCCAAT 519

RESULT 29

ACC85297
ID ACC85297 standard; cDNA; 1611 BP.

XX
AC ACC85297;

DT 18-SEP-2003 (first entry)

XX Arabidopsis cytokinin oxidase-like protein 5 cDNA #1.

DE Maize; root growth; root geotropism; cytokinin oxidase; seed size;
XX embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

KW Arabidopsis thaliana.

XX WO2003050287-A2.

PN 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.

XX 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2003-541577/51.

XX Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

XX Claim 3; Page 170-171; 177pp; English.

XX The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological

CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX

SQ Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;

Alignment Scores: 556 Length: 1611
Pred. No.: 35.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 9

US-10-014-101B-39 (1-7) x ACC85297 (1-1611)

QY 1 ValGlyGlyThrLeuSerAsn 7
DB 499 GTTGAGGTACACTCTCCAAT 519

RESULT 30

ABK28632

ID ABK28632 standard; cDNA; 1620 BP.

XX
AC ABK28632;

XX 09-APR-2002 (first entry)

XX CDNA encoding A. thaliana cytokinin oxidase AtCKX5 (long version).

KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;

KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX Arabidopsis thaliana.

PN WO200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

PR 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2002-130736/17.

XX P-PSDB; AAU81974.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.

XX Claim 3; Page 151; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size

CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX

SQ Sequence 1620 BP; 419 A; 380 C; 411 G; 410 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 559 Length: 1620
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x ABK28632 (1-1620)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 508 GTTGAGGTACACTCTCCAAT 528

RESULT 31
ACC85301
ID ACC85301 standard; cDNA; 1620 BP.
XX

AC ACC85301;

DT 18-SEP-2003 (first entry)

DE Arabidopsis cytokinin oxidase-like protein 5 cDNA #2.

XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX

OS Arabidopsis thaliana.

XX WO2003050287-A2.

PN 19-JUN-2003.

PD 10-DEC-2002; 2002WO-EP013990.

PF 10-DEC-2001; 2001US-00014101.

PR (SCHM/) SCHMULLING T.
XX (WERN/) WERNER T.

PA Schmullling T, Werner T;

XX WPI; 2003-541577/51.

DR Stimulating root growth, enhancing lateral or adventitious root formation
XX or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

PS Claim 3; Page 174-175; 177pp; English.

XX The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,

CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX

SQ Sequence 1620 BP; 419 A; 380 C; 411 G; 410 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 559 Length: 1620
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x ACC85301 (1-1620)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 508 GTTGAGGTACACTCTCCAAT 528

RESULT 32
ADH61271

ID ADH61271 standard; DNA; 1623 BP.

XX AC ADH61271;

DT 25-MAR-2004 (first entry)

XX Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #5.

DE Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX

OS Arabidopsis thaliana.

XX US2003163847-A1.

PD 28-AUG-2003.

XX 20-DEC-2002; 2002US-00326184.

XX 20-DEC-2001; 2001US-0343129P.

PR (PHAA) PHARMACIA CORP.

XX Huang S, Crossland LD, Cheikh N, Morris RO;

PI WPI; 2003-897983/82.
XX GENBANK; AF303982.

DR Producing plants characterized by reversible male-sterility, useful for
XX maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.

XX Claim 45; SEQ ID NO 12; 33pp; English.

PS The invention relates to a method for producing a plant characterised by
XX reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.

XX Sequence 1623 BP; 421 A; 382 C; 412 G; 408 T; 0 U; 0 Other;

SQ Alignment Scores:

Pred. No.: 560 Length: 1623
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-39 (1-7) x ADH61271. (1-1623)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 511 GTTGAGGTACACTCTCCAAT 531

RESULT 33

ADH61279

ID ADH61279 standard; DNA; 1655 BP.

XX

AC ADH61279;

XX

DT 25-MAR-2004 (first entry)

XX

DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #6.

XX

KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;

CKX1; mouse-ear cress; gene; ds.

XX

OS Arabidopsis thaliana.

XX

PN US2003163847-A1.

XX

PD 28-AUG-2003.

XX

PF 20-DEC-2002; 2002US-00326184.

XX

PR 20-DEC-2001; 2001US-0343129P.

XX

PA (PHAA) PHARMACIA CORP.

XX

PI Huang S, Crossland LD, Cheikh N, Morris RO;

XX

DR WPI; 2003-897983/82.

DR GENBANK; BT000179.

XX

PT Producing plants characterized by reversible male-sterility, useful for maintaining male sterility in plants, by transforming a plant cell with a nucleic acid construct containing a polynucleotide encoding a cytokinin oxidase.

XX

PS Disclosure; SEQ ID NO 20; 33pp; English.

XX

CC The invention relates to a method for producing a plant characterised by reversible male-sterility which involves transforming a plant cell with a nucleic acid construct containing a polynucleotide encoding a cytokinin oxidase. The method is useful for producing reversible male-sterility in transgenic plants, or for maintaining male sterility in plants. The method reduces the expense of seed production for existing hybrid plants such as corn, but also makes it possible to produce hybrid varieties of traditionally non-hybrid crops. The method is also useful for introducing economically valuable traits from plants having undesirable production characteristics into plants having desirable characteristics. The present sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This sequence is used to illustrate the method of the invention.

XX

SQ Sequence 1655 BP; 444 A; 380 C; 358 G; 473 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 573 Length: 1655
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-39 (1-7) x ADH61279 (1-1655)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 535 GTCGGGGGACGTTGTCCGAC 555

RESULT 34

ADA70177

ID ADA70177 standard; DNA; 1677 BP.

XX

AC ADA70177;

XX

DT 20-NOV-2003 (first entry)

XX

DE Rice gene, SEQ ID 3500.

XX

KW Plant; bacterial infection; fungal infection; viral infection; rice;

KW gene; ds.

XX

OS Oryza sativa.

XX

PN WO2003000898-A1.

XX

PD 03-JAN-2003.

XX

PF 22-JUN-2001; 2001WO-IB001105.

XX

PR 22-JUN-2001; 2001WO-IB001105.

XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX

DR WPI; 2003-175290/17.

XX

PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX

PS Claim 6; SEQ ID NO 3500; 899pp; English.

XX

CC The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

XX

SQ Sequence 1677 BP; 219 A; 608 C; 582 G; 267 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 581 Length: 1677
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x ADA70177 (1-1677)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 532 GTCGGGGGACGCTGTCCAC 552

RESULT 35

ADS49453/C

ID ADS49453 standard; CDNA; 1719 BP.

XX ADS49453;
AC
XX
DT 02-DEC-2004 (first entry)
XX Bacterial polynucleotide #4196.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
XX US2003233675-A1.
PN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI
XX WPI; 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 27883; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1719 BP; 413 A; 466 C; 489 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 597 Length: 1719
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-014-101B-39 (1-7) x ADS49453 (1-1719)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 503 GTAGCGGGACGCTCTCAAAC 483
RESULT 36
ABK28624
ID ABK28624 standard; cDNA; 1728 BP.
XX
AC ABK28624;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX1.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX
OS Arabidopsis thaliana.
XX
XX WO200196580-A2.
PN
XX
PD 20-DEC-2001.
XX
XX 18-JUN-2001; 2001WO-EP006833.
PF
XX 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
PA
XX Schmulling T, Werner T;
PI
XX WPI; 2002-130736/17.
DR
XX

Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 146; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX

Sequence 1728 BP; 544 A; 390 C; 332 G; 462 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 601 Length: 1728
Score: 35.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x ABK28624 (1-1728)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 574 GTTGAGGTACACTATCTAAT 594

RESULT 37

ACC85293

ID ACC85293 standard; cDNA; 1728 BP.

XX

AC ACC85293;

XX

DT 18-SEP-2003 (first entry)

XX

DE Arabidopsis cytokinin oxidase-like protein 1 cDNA.

XX

KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;

KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

XX

OS Arabidopsis thaliana.

XX

PN WO2003050287-A2.

XX

PD 19-JUN-2003.

XX

PF 10-DEC-2002; 2002WO-EP013990.

XX

PR 10-DEC-2001; 2001US-00014101.

XX

PA (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX

PI Schmullling T, Werner T;

XX

DR WPI; 2003-541577/51.

XX

PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

XX

PS Claim 122; Page 166-167; 177pp; English.

XX

CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention

XX

SQ Sequence 1728 BP; 544 A; 390 C; 332 G; 462 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 601 Length: 1728
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x ACC85293 (1-1728)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 574 GTTGAGGTACACTATCTAAT 594

RESULT 38

ADO06496

ID ADO06496 standard; DNA; 1728 BP.

XX

AC ADO06496;

XX

DT 29-JUL-2004 (first entry)

XX

DE A thaliana cytokinin oxidase AtCKX1 coding sequence.

XX

KW bioremediation; AtCKX1; cytokinin availability; contaminant;

KW metal deficiency; nutrition; ds; gene; cytokinin oxidase.

XX

OS Arabidopsis thaliana.

XX

FH Key Location/Qualifiers

FT CDS 1..1728

FT /*tag= a

FT /product= "cytokinin oxidase AtCKX1"

XX

PN WO2004038027-A1.

XX

PD 06-MAY-2004.

XX

PF 24-OCT-2003; 2003WO-EP012051.

XX

PR 24-OCT-2002; 2002EP-00079481.

XX

PA (CROP-) CROPDESIGN NV.

XX

PI Van Camp W;

XX

DR WPI; 2004-375913/35.

DR

P-PSDB; ADO06497.

XX

PT Method for bioremediation, useful for removing contaminants or metals, by
PT decreasing cytokinin availability in plants, and cultivating plant on
PT substrate comprising one or more contaminants.

XX

PS Claim 8; Page 53; 61pp; English.

XX

CC The present invention relates to a method for bioremediation, which
CC involves decreasing cytokinin availability in a plant relative to a
CC corresponding wild type plant, and cultivating the plant on a substrate
CC comprising one or more contaminants, or cultivating a plant having
CC lowered availability of cytokinin relative to corresponding wild type
CC plants, on a substrate, which is to be treated. The method is useful for
CC bioremediation, for concentration of contaminants in a plant, where the
CC plant has a higher concentration of contaminants compared to a
CC corresponding wild type plant. The metal contaminants include aluminum,
CC americium, antimony, arsenic, barium, beryllium, bismuth, cadmium,
CC caesium, cerium, chromium, copper, gallium, germanium, gold, indium,
CC iridium, iron, lead, manganese, mercury, molybdenum, neptunium, osmium,
CC palladium, platinum, plutonium, radium, rhenium, rhodium, rubidium,
CC ruthenium, scandium, selenium, silver, strontium, technetium, tellurium,
CC thallium, tin, tungsten, uranium, vanadium, yttrium, preferably
CC cadmium. The plant obtained by the method is useful in bioremediation.
CC Transgenic plants with a lower availability of cytokinin are useful in
CC the manufacture of a medicament for treatment of disorders arising from
CC metal deficiencies, and as a medicament for improving animal or human
CC nutrition. The present sequence is a coding sequence shown in the
CC exemplification of the invention.

XX

SQ Sequence 1728 BP; 544 A; 390 C; 332 G; 462 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 601 Length: 1728
Score: 35.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-39 (1-7) x ADO06496 (1-1728)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 574 GTTGGAGGTACACTATCTAAT 594

RESULT 39

ADH61281
ID ADH61281 standard; DNA; 1857 BP.
XX
AC ADH61281;
XX
DT 25-MAR-2004 (first entry)
XX
DE Barley cytokinin oxidase (CKX1) DNA #1.
XX

KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; barley; ds; gene.
XX

OS Hordeum vulgare.
XX

PN US2003163847-A1.
XX

PD 28-AUG-2003.
XX

PF 20-DEC-2002; 2002US-00326184.
XX

PR 20-DEC-2001; 2001US-0343129P.
XX

PA (PHAA) PHARMACIA CORP.
XX

PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX

DR WPI; 2003-897983/82.
DR GENBANK; AF540382.
XX

PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX

PS Disclosure; SEQ ID NO 22; 33pp; English.
XX

CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is barley cytokinin oxidase (CKX1) DNA. This sequence is used to
CC illustrate the method of the invention.
XX

SQ Sequence 1857 BP; 521 A; 454 C; 437 G; 445 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 651 Length: 1857
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-39 (1-7) x ADH61281 (1-1857)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 590 GTTGGGGGCACGTTGTCAAAT 610
RESULT 40
ADH61280
ID ADH61280 standard; DNA; 1873 BP.
XX
AC ADH61280;
XX
DT 25-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #7.
XX

KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; mouse-ear cress; gene; ds.
XX

OS Arabidopsis thaliana.
XX

PN US2003163847-A1.
XX

PD 28-AUG-2003.
XX

PF 20-DEC-2002; 2002US-00326184.
XX

PR 20-DEC-2001; 2001US-0343129P.
XX

PA (PHAA) PHARMACIA CORP.
XX

PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX
DR WPI; 2003-897983/82.
DR GENBANK; AY091158.
XX

PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX

PS Disclosure; SEQ ID NO 21; 33pp; English.
XX

CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is Arabidopsis thaliana cytokinin oxidase (CKX1) DNA. This
CC sequence is used to illustrate the method of the invention.
XX

SQ Sequence 1873 BP; 495 A; 385 C; 482 G; 511 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 657 Length: 1873
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-39 (1-7) x ADH61280 (1-1873)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 617 GTGGAGGTACGTTGTCAAAT 637

Search completed: February 18, 2005, 03:26:38
Job time : 129.02 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 02:33:38 ; Search time 41.3 Seconds
(without alignments)
277.335 Million cell updates/sec

Title: US-10-014-101B-39
Perfect score: 35
Sequence: 1 VGGTSLN 7

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101 @CGN 1 1 124 @runat 16022005 075846 7970 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA:*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	35	100.0	442	US-09-513-999C-2604	Sequence 2604, Ap
2	35	100.0	1605	US-09-124-541-3	Sequence 3, Appli
3	35	100.0	1605	US-09-663-326-3	Sequence 3, Appli
4	35	100.0	6733	US-09-124-541-2	Sequence 2, Appli
5	35	100.0	6733	US-09-663-326-2	Sequence 2, Appli
6	34	97.1	129127	US-09-949-016-13481	Sequence 13481, A
C 7	33	94.3	2828	US-09-949-016-3718	Sequence 3718, Ap
C 8	33	94.3	41754	US-09-949-016-15460	Sequence 15460, A
C 9	32	91.4	548	US-09-270-767-560	Sequence 560, App
C 10	32	91.4	548	US-09-270-767-15842	Sequence 15842, A
11	32	91.4	601	US-09-949-016-163961	Sequence 163961,
12	32	91.4	601	US-09-949-016-163962	Sequence 163962,

13	32	91.4	8885	4	US-09-634-238-26	Sequence 26, Appl
14	32	91.4	49931	4	US-09-949-016-13727	Sequence 13727, A
15	32	91.4	49931	4	US-09-949-016-13728	Sequence 13728, A
16	32	91.4	49931	4	US-09-949-016-13729	Sequence 13729, A
17	32	91.4	49971	4	US-09-949-016-16688	Sequence 16688, A
18	32	91.4	94830	4	US-09-949-016-12414	Sequence 12414, A
19	32	91.4	94847	4	US-09-949-016-16336	Sequence 16336, A
20	32	91.4	130298	4	US-09-949-016-16664	Sequence 16664, A
21	32	91.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
22	32	91.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 23	31	88.6	363	4	US-09-614-221A-253	Sequence 253, App
C 24	31	88.6	473	4	US-09-471-276-723	Sequence 723, App
C 25	31	88.6	506	4	US-09-536-059-5	Sequence 5, Appli
C 26	31	88.6	562	4	US-09-621-976-338	Sequence 338, App
C 27	31	88.6	891	4	US-09-543-681A-1481	Sequence 1481, Ap
C 28	31	88.6	972	4	US-09-328-352-1982	Sequence 1982, Ap
29	31	88.6	1155	4	US-09-543-681A-2172	Sequence 2172, Ap
30	31	88.6	1273	4	US-09-270-767-14731	Sequence 14731, A
C 31	31	88.6	1831	3	US-09-433-248A-5	Sequence 5, Appli
32	31	88.6	1877	2	US-08-634-924B-1	Sequence 1, Appli
33	31	88.6	1877	4	US-09-395-554-1	Sequence 1, Appli
34	31	88.6	1877	4	US-09-395-554-3	Sequence 3, Appli
C 35	31	88.6	2727	4	US-09-248-796A-638	Sequence 638, App
C 36	31	88.6	14231	3	US-08-961-527-81	Sequence 81, Appl
C 37	31	88.6	19181	4	US-09-949-016-15016	Sequence 15016, A
C 38	31	88.6	26928	4	US-09-544-398B-6	Sequence 6, Appli
C 39	31	88.6	26928	4	US-09-543-771B-6	Sequence 6, Appli
C 40	31	88.6	44342	4	US-09-949-016-12661	Sequence 12661, A
C 41	31	88.6	47787	4	US-09-949-016-11969	Sequence 11969, A
C 42	31	88.6	62804	3	US-09-800-960-3	Sequence 3, Appli
C 43	31	88.6	62804	4	US-10-096-960-3	Sequence 3, Appli
44	31	88.6	76401	4	US-09-949-016-17153	Sequence 17153, A
45	31	88.6	94755	4	US-09-949-016-11839	Sequence 11839, A

ALIGNMENTS

RESULT 1

US-09-513-999C-2604/c
; Sequence 2604, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2604
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126...440
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 32
; OTHER INFORMATION: k=g or t
US-09-513-999C-2604

Alignment Scores:
Pred. No.: 26.3 Length: 442
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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DB: 4 Gaps: 0
US-10-014-101B-39 (1-7) x US-09-513-999C-2604 (1-442)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 67 GTGGGCGGAACGCTTTCTAAT 47
RESULT 2
US-09-124-541-3
; Sequence 3, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-124-541-3
Alignment Scores:
Pred. No.: 113 Length: 1605
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-014-101B-39 (1-7) x US-09-124-541-3 (1-1605)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 523 GTGGGCGGACGCTGTCCAAC 543
RESULT 3
US-09-663-326-3
; Sequence 3, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-663-326-3
Alignment Scores:
Pred. No.: 113 Length: 1605
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-39 (1-7) x US-09-663-326-3 (1-1605)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 523 GTGGGCGGACGCTGTCCAAC 543
RESULT 4
US-09-124-541-2
; Sequence 2, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-124-541-2
Alignment Scores:
Pred. No.: 571 Length: 6733
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-014-101B-39 (1-7) x US-09-124-541-2 (1-6733)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 2019 GTGGGCGGACGCTGTCCAAC 2039
RESULT 5
US-09-663-326-2
; Sequence 2, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-663-326-2

Alignment Scores:
Pred. No.: 571 Length: 6733
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-663-326-2 (1-6733)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 2019 GTCGGCGGCACGCTGTCCAAC 2039

RESULT 6
US-09-949-016-13481
; Sequence 13481, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13481
; LENGTH: 129127
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13481

Alignment Scores:
Pred. No.: 2.73e+04 Length: 129127
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 97.14% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-13481 (1-129127)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 104757 ATAGGAGGACACTTAGCAAT 104777
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RESULT 7
US-09-949-016-3718/c
; Sequence 3718, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3718
; LENGTH: 2828
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3718

Alignment Scores:
Pred. No.: 626 Length: 2828
Score: 33.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 94.29% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-3718 (1-2828)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 1446 GTAGGAGGAACAATATCTAAT 1426

RESULT 8
US-09-949-016-15460/c
; Sequence 15460, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15460
; LENGTH: 41754
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15460

Alignment Scores:
Pred. No.: 1.31e+04 Length: 41754
Score: 33.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 94.29% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-15460 (1-41754)
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QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 26813 GTAGGAGGAACAATATCTAAT 26793

RESULT 9
US-09-270-767-560/c
; Sequence 560, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 560
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-560

Alignment Scores:
Pred. No.: 168 Length: 548
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-270-767-560 (1-548)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 25 GTTGGTGGGACGTTGACTAAT 5

RESULT 10
US-09-270-767-15842/c
; Sequence 15842, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15842
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15842

Alignment Scores:
Pred. No.: 168 Length: 548
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-270-767-15842 (1-548)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 25 GTTGGTGGGACGTTGACTAAT 5

RESULT 11.
US-09-949-016-163961
; Sequence 163961, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163961
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-163961

Alignment Scores:
Pred. No.: 186 Length: 601
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-163961 (1-601)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 516 GTTGGAGGAACCTTTAGCCAAC 536

RESULT 12
US-09-949-016-163962
; Sequence 163962, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163962
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-163962

Alignment Scores:
Pred. No.: 186 Length: 601
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-163962 (1-601)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 397 GTTGGAGGAACCTTTAGCCAAC 417

RESULT 13
US-09-634-238-26
; Sequence 26, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 8885
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-26

Alignment Scores:
Pred. No.: 3.9e+03 Length: 8885
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-634-238-26 (1-8885)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 3064 GTGGTGGAACCGTCAGCAAC 3084

RESULT 14
US-09-949-016-13727
; Sequence 13727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13727
; LENGTH: 49931
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49931)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13727
Alignment Scores:

Pred. No.: 2.73e+04 Length: 49931
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-39 (1-7) x US-09-949-016-13727 (1-49931)
Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 20294 GTTGAGGAACGCTAAACAAT 20314
RESULT 15
US-09-949-016-13728
; Sequence 13728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13728
; LENGTH: 49931
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49931)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13728

Alignment Scores:
Pred. No.: 2.73e+04 Length: 49931
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-13728 (1-49931)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 20294 GTTGAGGAACGCTAAACAAT 20314

RESULT 16
US-09-949-016-13729
; Sequence 13729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13727
; LENGTH: 49931
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49931)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13727
Alignment Scores:

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13729
; LENGTH: 49931
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49931)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13729

Alignment Scores:
Pred. No.: 2.73e+04 Length: 49931
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-13729 (1-49931)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 20294 GTTGGAGGACGCTAACAAT 20314

RESULT 17

US-09-949-016-16688
; Sequence 16688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16688
; LENGTH: 49971
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49971)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16688

Alignment Scores:
Pred. No.: 2.73e+04 Length: 49971
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-16688 (1-49971)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 32992 CTGGAGGCACACTTAGTAAC 33012

RESULT 18

US-09-949-016-12414
; Sequence 12414, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12414
; LENGTH: 94830
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12414

Alignment Scores:
Pred. No.: 5.6e+04 Length: 94830
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-12414 (1-94830)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 39706 GTTGGAGGAACCTTAGCCAAC 39726

RESULT 19

US-09-949-016-16336
; Sequence 16336, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16336
; LENGTH: 94847
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16336

Alignment Scores:
Pred. No.: 5.6e+04 Length: 94847
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 91.43% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-949-016-16336 (1-94847)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 39706 GTTGGAGGAACCTTAGCCAAC 39726

US-10-014-101B-39 (1-7) x US-09-614-221A-253 (1-363)

Qy 2 GlyGlyThrLeuSerAsn 7
Db 199 GGTGGCACCTTGTC CAAT 182

RESULT 24

US-09-471-276-723/c
; Sequence 723, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 723
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 63..473
; NAME/KEY: sig_peptide
; LOCATION: 63..212
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.5
; OTHER INFORMATION: seq ITYGVFLCIDCSG/SH
US-09-471-276-723

Alignment Scores:
Pred. No.: 243 Length: 473
Score: 31.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.57% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-471-276-723 (1-473)

Qy 2 GlyGlyThrLeuSerAsn 7
Db 219 GGTGGACCCCTGAGCAAT 202

RESULT 25

US-09-536-059-5/c
; Sequence 5, Application US/09536059
; Patent No. 6544737
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen-Akenine, Annick
; TITLE OF INVENTION: GENOMIC SEQUENCE OF THE purH GENE AND purH-RELATED BIALLELIC
; TITLE OF INVENTION: MARKERS.
; FILE REFERENCE: GENSET.058AUS
; CURRENT APPLICATION NUMBER: US/09/536,059
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/125,961
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72
; OTHER INFORMATION: 99-22580-72 : polymorphic base A or T
; NAME/KEY: misc_binding
; LOCATION: 60..84
; OTHER INFORMATION: 99-22580-72.probe
; NAME/KEY: primer_bind
; LOCATION: 53..71
; OTHER INFORMATION: 99-22580-72.mis
; NAME/KEY: primer_bind
; LOCATION: 73..91
; OTHER INFORMATION: 99-22580-72.mis complement
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: 99-22580.pu
; NAME/KEY: primer_bind
; LOCATION: 488..506
; OTHER INFORMATION: 99-22580.rp complement
US-09-536-059-5

Alignment Scores:
Pred. No.: 262 Length: 506
Score: 31.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.57% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-536-059-5 (1-506)

Qy 2 GlyGlyThrLeuSerAsn 7
Db 332 GGAGGTACTCTCTTAAC 315

RESULT 26

US-09-621-976-338/c
; Sequence 338, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 338
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 292..561
; NAME/KEY: sig_peptide
; LOCATION: 292..489
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.79999995231628
; OTHER INFORMATION: seq LWLDSCVVPLSP/PP
US-09-621-976-338

Alignment Scores:
Pred. No.: 295 Length: 562
Score: 31.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.57% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-621-976-338 (1-562)

Qy 2 GlyGlyThrLeuSerAsn 7

Db 214 GGTGGACCTGAGCAAT 197

RESULT 27

US-09-543-681A-1481/c

; Sequence 1481, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 1481

; LENGTH: 891

; TYPE: DNA

; ORGANISM: Proteus mirabilis

US-09-543-681A-1481

Alignment Scores:

Pred. No.: 496 Length: 891

Score: 31.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.57% Indels: 0

DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-543-681A-1481 (1-891)

Qy 2 GlyGlyThrLeuSerAsn 7

Db 743 GCGGAACATTGAGTAAC 726

RESULT 28

US-09-328-352-1982

; Sequence 1982, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 1982

; LENGTH: 972

; TYPE: DNA

; ORGANISM: Acinetobacter baumannii

US-09-328-352-1982

Alignment Scores:

Pred. No.: 548 Length: 972

Score: 31.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.57% Indels: 0

DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-328-352-1982 (1-972)

Qy 2 GlyGlyThrLeuSerAsn 7

Db 214 GGTGGACCTGAGCAAT 197

Db 613 GGTGGAACATTATCGAAT 630

RESULT 29

US-09-543-681A-2172

; Sequence 2172, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 2172

; LENGTH: 1155

; TYPE: DNA

; ORGANISM: Proteus mirabilis

US-09-543-681A-2172

Alignment Scores:

Pred. No.: 665 Length: 1155

Score: 31.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.57% Indels: 0

DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-543-681A-2172 (1-1155)

Qy 2 GlyGlyThrLeuSerAsn 7

Db 988 GGTGACATTGAGTAAT 1005

RESULT 30

US-09-270-767-14731

; Sequence 14731, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14731

; LENGTH: 1273

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-09-270-767-14731

Alignment Scores:

Pred. No.: 743 Length: 1273

Score: 31.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.57% Indels: 0

DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-270-767-14731 (1-1273)

Qy 2 GlyGlyThrLeuSerAsn 7

Db 787 GGAGGTACTCTTTCAAT 804

RESULT 31

US-09-433-248A-5/c

; Sequence 5, Application US/09433248A

; Patent No. 6355462

; GENERAL INFORMATION:

```
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Han, Feng
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Disease Resistance Factors
; FILE REFERENCE: BB1252 US NA
; CURRENT APPLICATION NUMBER: US/09/433,248A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,242
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Glycine max
US-09-433-248A-5

Alignment Scores:
Pred. No.:      1.12e+03      Length:      1831
Score:          31.00        Matches:      5
Percent Similarity: 100.00%    Conservative: 2
Best Local Similarity: 71.43%  Mismatches:      0
Query Match:    88.57%        Indels:        0
DB:              3          Gaps:          0

US-10-014-101B-39 (1-7) x US-09-433-248A-5 (1-1831)

QY      1 ValGlyGlyThrLeuSerAsn 7
      :::|||||:::
Db      759 ATAGTGGAACCTGTGACCAAC 739

RESULT 32
US-08-634-924B-1
; Sequence 1, Application US/08634924B
; Patent No. 5834419
; GENERAL INFORMATION:
; APPLICANT: MCFADDEN, GRANT
; APPLICANT: LUCAS, ALEXANDRA
; TITLE OF INVENTION: CHEMOKINE BINDING PROTEIN AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,924B
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,850
; FILING DATE: 19-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.,
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: PD-3675
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1877 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CBP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 455..1243
US-08-634-924B-1

Alignment Scores:
Pred. No.:      1.15e+03      Length:      1877
Score:          31.00        Matches:      5
Percent Similarity: 100.00%    Conservative: 2
Best Local Similarity: 71.43%  Mismatches:      0
Query Match:    88.57%        Indels:        0
DB:              2          Gaps:          0

US-10-014-101B-39 (1-7) x US-08-634-924B-1 (1-1877)

QY      1 ValGlyGlyThrLeuSerAsn 7
      :::|||||:::
Db      1180 ATTGGAGGAACGTGTATCTAAC 1200

RESULT 33
US-09-395-554-1
; Sequence 1, Application US/09395554
; Patent No. 6495515
; GENERAL INFORMATION:
; APPLICANT: MCFADDEN, GRANT
; APPLICANT: LUCAS, ALEXANDRA
; TITLE OF INVENTION: CHEMOKINE BINDING PROTEIN AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: 50082/002004
; CURRENT APPLICATION NUMBER: US/09/395,554
; CURRENT FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 09/181,122
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 08/634,924
; EARLIER FILING DATE: 1996-04-19
; EARLIER APPLICATION NUMBER: 08/424,850
; EARLIER FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Myxoma virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (455) ... (1243)
US-09-395-554-1

Alignment Scores:
Pred. No.:      1.15e+03      Length:      1877
Score:          31.00        Matches:      5
Percent Similarity: 100.00%    Conservative: 2
Best Local Similarity: 71.43%  Mismatches:      0
Query Match:    88.57%        Indels:        0
DB:              4          Gaps:          0

US-10-014-101B-39 (1-7) x US-09-395-554-1 (1-1877)

QY      1 ValGlyGlyThrLeuSerAsn 7
      :::|||||:::
Db      1180 ATTGGAGGAACGTGTATCTAAC 1200

RESULT 34
US-09-395-554-3
; Sequence 3, Application US/09395554
; Patent No. 6495515
; GENERAL INFORMATION:
; APPLICANT: MCFADDEN, GRANT
; APPLICANT: LUCAS, ALEXANDRA
```

```

; TITLE OF INVENTION: CHEMOKINE BINDING PROTEIN AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: 50082/002004
; CURRENT APPLICATION NUMBER: US/09/395,554
; CURRENT FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 09/181,122
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 08/634,924
; EARLIER FILING DATE: 1996-04-19
; EARLIER APPLICATION NUMBER: 08/424,850
; EARLIER FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Myxoma virus
US-09-395-554-3

Alignment Scores:
Pred. No.: 1.15e+03 Length: 1877
Score: 31.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 88.57% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-395-554-3 (1-1877)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 1180 ATTGGAGGAAGTGTATCTAAC 1200

RESULT 35
US-09-248-796A-638/c
; Sequence 638, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RE
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 638
; LENGTH: 2727
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-638

Alignment Scores:
Pred. No.: 1.76e+03 Length: 2727
Score: 31.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 88.57% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-248-796A-638 (1-2727)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 2529 ATTGGAGGACGGTAAGTAAC 2509

RESULT 36
US-08-961-527-81/c
; Sequence 81, Application US/08961527
; Patent No. 6420135

```



```

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15016

Alignment Scores:
Pred. No.: 1.59e+04 19181
Score: 31.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 88.57% 0
DB: 4 0

US-10-014-101B-39 (1-7) x US-09-949-016-15016 (1-19181)

QY 2 GlyGlyThrLeuSerAsn 7
Db 4973 GGTGGAACACTTTCAAAT 4990

RESULT 38
US-09-544-398B-6/c
; Sequence 6, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 26928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12044), (12489), (26433), (26434), (26435), (26436), (26439), (26441)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-544-398B-6

Alignment Scores:
Pred. No.: 2.33e+04 26928
Score: 31.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 88.57% 0
DB: 4 0

US-10-014-101B-39 (1-7) x US-09-544-398B-6 (1-26928)

QY 2 GlyGlyThrLeuSerAsn 7
Db 18890 GGTGGACCCCTCTCCAAT 18873

RESULT 39
US-09-543-771B-6/c
; Sequence 6, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
```

```

; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 26928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12044), (12489), (26433), (26434), (26435), (26436), (26439), (26441)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-543-771B-6

Alignment Scores:
Pred. No.: 2.33e+04 26928
Score: 31.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 88.57% 0
DB: 4 0

US-10-014-101B-39 (1-7) x US-09-543-771B-6 (1-26928)

QY 2 GlyGlyThrLeuSerAsn 7
Db 18890 GGTGGACCCCTCTCCAAT 18873

RESULT 40
US-09-949-016-12661/c
; Sequence 12661, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12661
; LENGTH: 44342
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12661

Alignment Scores:
Pred. No.: 4.07e+04 44342
Score: 31.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 88.57% 0
DB: 4 0

US-10-014-101B-39 (1-7) x US-09-949-016-12661 (1-44342)

QY 2 GlyGlyThrLeuSerAsn 7
Db 16570 GGTGGACCCCTGAGCAAT 16553
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Search completed: February 18, 2005, 07:16:11
Job time : 586.55 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
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Perfect score: 35
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5384158 seqs, 2955248155 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	100.0	470	18	US-10-425-115-168063	Sequence 168063,
2	35	100.0	566	16	US-10-326-184-14	Sequence 14, Appl
3	35	100.0	579	18	US-10-021-323-14076	Sequence 14076, A
4	35	100.0	641	18	US-10-021-323-8905	Sequence 8905, Ap
5	35	100.0	718	17	US-10-424-599-69520	Sequence 69520, A
6	35	100.0	840	18	US-10-425-115-35579	Sequence 35579, A
7	35	100.0	955	18	US-10-425-115-35581	Sequence 35581, A
8	35	100.0	1142	17	US-10-425-114-8251	Sequence 8251, Ap
9	35	100.0	1318	17	US-10-424-599-9802	Sequence 9802, Ap
10	35	100.0	1318	17	US-10-424-599-12845	Sequence 12845, A
11	35	100.0	1384	17	US-10-425-114-8799	Sequence 8799, Ap
12	35	100.0	1506	14	US-10-014-101-26	Sequence 26, Appl
13	35	100.0	1506	17	US-10-311-453-26	Sequence 26, Appl
14	35	100.0	1515	14	US-10-014-101-30	Sequence 30, Appl
15	35	100.0	1515	17	US-10-311-453-30	Sequence 30, Appl
16	35	100.0	1560	18	US-10-817-483-26	Sequence 26, Appl
17	35	100.0	1566	18	US-10-817-483-30	Sequence 30, Appl
18	35	100.0	1572	14	US-10-014-101-27	Sequence 27, Appl
19	35	100.0	1572	16	US-10-326-184-9	Sequence 9, Appli
20	35	100.0	1572	17	US-10-311-453-27	Sequence 27, Appl
21	35	100.0	1575	9	US-09-938-842A-2089	Sequence 2089, Ap
22	35	100.0	1575	11	US-09-938-842A-2089	Sequence 2089, Ap
23	35	100.0	1575	14	US-10-014-101-28	Sequence 28, Appl
24	35	100.0	1575	16	US-10-326-184-10	Sequence 10, Appl
25	35	100.0	1575	16	US-10-326-184-11	Sequence 11, Appl
26	35	100.0	1575	17	US-10-311-453-28	Sequence 28, Appl
27	35	100.0	1599	18	US-10-437-963-88564	Sequence 88564, A
28	35	100.0	1605	18	US-10-437-963-38170	Sequence 38170, A
29	35	100.0	1605	18	US-10-821-711-4	Sequence 4, Appli
30	35	100.0	1605	18	US-10-821-711-5	Sequence 5, Appli
31	35	100.0	1611	14	US-10-014-101-29	Sequence 29, Appl
32	35	100.0	1611	17	US-10-311-453-29	Sequence 29, Appl
33	35	100.0	1617	18	US-10-817-483-28	Sequence 28, Appl
34	35	100.0	1620	14	US-10-014-101-34	Sequence 34, Appl
35	35	100.0	1620	17	US-10-311-453-34	Sequence 34, Appl
36	35	100.0	1623	16	US-10-326-184-12	Sequence 12, Appl
37	35	100.0	1629	18	US-10-817-483-32	Sequence 32, Appl
38	35	100.0	1655	16	US-10-326-184-20	Sequence 20, Appl
39	35	100.0	1670	18	US-10-437-963-70571	Sequence 70571, A
40	35	100.0	1673	18	US-10-437-963-83827	Sequence 83827, A
41	35	100.0	1677	18	US-10-437-963-43981	Sequence 43981, A
42	35	100.0	1718	18	US-10-437-963-86803	Sequence 86803, A
43	35	100.0	1719	17	US-10-369-493-27883	Sequence 27883, A
44	35	100.0	1728	14	US-10-014-101-25	Sequence 25, Appl
45	35	100.0	1728	17	US-10-311-453-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-425-115-168063
; Sequence 168063, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 168063
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (1)..(470)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_84854C.1
US-10-425-115-168063

Alignment Scores:
Pred. No.: 156 Length: 470
Score: 35.00 Matches: 7
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 18 Indels: 0
Gaps: 0

US-10-014-101B-39 (1-7) x US-10-425-115-168063 (1-470)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 295 GTGGCGGCACGCTCTCCAAT 315

RESULT 2

US-10-326-184-14
; Sequence 14, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:

; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Glycine max
US-10-326-184-14

Alignment Scores:
Pred. No.: 188 Length: 566
Score: 35.00 Matches: 7
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 16 Indels: 0
Gaps: 0

US-10-014-101B-39 (1-7) x US-10-326-184-14 (1-566)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 133 GTGGGAGGACACTTTTCCAAT 153

RESULT 3

US-10-021-323-14076
; Sequence 14076, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:

; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880

; SEQ ID NO 14076
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(579)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-029-Q6-K6-G4
US-10-021-323-14076

Alignment Scores:
Pred. No.: 193 Length: 579
Score: 35.00 Matches: 7
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 18 Indels: 0
Gaps: 0

US-10-014-101B-39 (1-7) x US-10-021-323-14076 (1-579)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 209 GTTGGTGAACCTTGTCTAAC 229

RESULT 4

US-10-021-323-8905
; Sequence 8905, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:

; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8905
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-021-Q1-K6-C8
US-10-021-323-8905

Alignment Scores:
Pred. No.: 213 Length: 641
Score: 35.00 Matches: 7
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 18 Indels: 0
Gaps: 0

US-10-014-101B-39 (1-7) x US-10-021-323-8905 (1-641)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 541 GTTGGTGAACCTTGTCTAAC 561

RESULT 5

US-10-424-599-69520
; Sequence 69520, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

```
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 69520
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33789C.1
US-10-424-599-69520

Alignment Scores:
Pred. No.:      239      Length:      718
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels:      0
DB:              17      Gaps:      0

US-10-014-101B-39 (1-7) x US-10-424-599-69520 (1-718)

Qy      1 ValGlyGlyThrLeuSerAsn 7
      |||||
Db      650 GTTGGTGGCACTCTCTCCAAC 670

RESULT 6
US-10-425-115-35579
; Sequence 35579, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 35579
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(840)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_132446C.1
US-10-425-115-35579

Alignment Scores:
Pred. No.:      279      Length:      840
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels:      0
DB:              18      Gaps:      0

US-10-014-101B-39 (1-7) x US-10-425-115-35579 (1-840)

Qy      1 ValGlyGlyThrLeuSerAsn 7
      |||||
Db      497 GTCGGTGGCACCTTGCTCTAAT 517

RESULT 7
US-10-425-115-35581
; Sequence 35581, Application US/10425115
; Publication No. US20040214272A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 35581
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(955)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_132448C.1
US-10-425-115-35581

Alignment Scores:
Pred. No.:      318      Length:      955
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels:      0
DB:              18      Gaps:      0

US-10-014-101B-39 (1-7) x US-10-425-115-35581 (1-955)

Qy      1 ValGlyGlyThrLeuSerAsn 7
      |||||
Db      680 GTCGGTGGCACCTTGCTCTAAT 700

RESULT 8
US-10-425-114-8251
; Sequence 8251, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8251
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700742678_FLI
US-10-425-114-8251

Alignment Scores:
Pred. No.:      380      Length:      1142
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels:      0
DB:              17      Gaps:      0

US-10-014-101B-39 (1-7) x US-10-425-114-8251 (1-1142)

Qy      1 ValGlyGlyThrLeuSerAsn 7
```

Db129GTCGGGGGACGCTCTCCAAT149

RESULT 9

US-10-424-599-9802

Sequence 9802, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 9802

LENGTH: 1318

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_108862C.1

US-10-424-599-9802

Alignment Scores:

Pred. No.:438Length:1318

Score:35.00Matches:7

Percent Similarity:100.00%Conservative:0

Best Local Similarity:100.00%Mismatches:0

Query Match:100.00%Indels:0

DB:17Gaps:0

US-10-014-101B-39 (1-7) x US-10-424-599-9802 (1-1318)

QY1ValGlyGlyThrLeuSerAsn7

Db628GTCGGAGGGACACTTCCAAT648

RESULT 10

US-10-424-599-12845

Sequence 12845, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 12845

LENGTH: 1318

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(1318)

OTHER INFORMATION: unsure at all n locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_111605C.1

US-10-424-599-12845

Alignment Scores:

Pred. No.:438Length:1318

Score:35.00Matches:7

Percent Similarity:100.00%Conservative:0

Best Local Similarity:100.00%Mismatches:0

Query Match:100.00%Indels:0

DB:17Gaps:0

US-10-014-101B-39 (1-7) x US-10-424-599-9802 (1-1318)

QY1ValGlyGlyThrLeuSerAsn7

Db628GTCGGAGGGACACTTCCAAT648

DB:17Gaps:0

US-10-014-101B-39 (1-7) x US-10-424-599-12845 (1-1318)

QY1ValGlyGlyThrLeuSerAsn7

Db664GTTGGGGGTACTCTTTCCAAT684

RESULT 11

US-10-425-114-8799

Sequence 8799, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 8799

LENGTH: 1384

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: 700793982_FLI

US-10-425-114-8799

Alignment Scores:

Pred. No.:460Length:1384

Score:35.00Matches:7

Percent Similarity:100.00%Conservative:0

Best Local Similarity:100.00%Mismatches:0

Query Match:100.00%Indels:0

DB:17Gaps:0

US-10-014-101B-39 (1-7) x US-10-425-114-8799 (1-1384)

QY1ValGlyGlyThrLeuSerAsn7

Db92GTCGGGGGACGCTCTCCAAT112

RESULT 12

US-10-014-101-26

Sequence 26, Application US/10014101

Publication No. US20030074698A1

GENERAL INFORMATION:

APPLICANT: Schmullling, Thomas

APPLICANT: Werner, Tom s

TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and

TITLE OF INVENTION: physiology

FILE REFERENCE: 1195-2

CURRENT APPLICATION NUMBER: US/10/014,101

CURRENT FILING DATE: 2001-12-10

PRIOR APPLICATION NUMBER: PCT/EP01/06833

PRIOR FILING DATE: 2001-06-16

PRIOR APPLICATION NUMBER: EP 00870132.8

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/258,415

PRIOR FILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: EP 01870053.4

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26

LENGTH: 1506

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-10-014-101-26
Alignment Scores:
Pred. No.: 501 Length: 1506
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-014-101-26 (1-1506)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGGAGGAACGTTGTCTGAAT 486

RESULT 13

US-10-311-453-26
; Sequence 26, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom 8
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-26

Alignment Scores:
Pred. No.: 501 Length: 1506
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-311-453-26 (1-1506)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 466 GTCGGAGGAACGTTGTCTGAAT 486

RESULT 14

US-10-014-101-30
; Sequence 30, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom 8
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415

; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-30

Alignment Scores:
Pred. No.: 504 Length: 1515
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-014-101-30 (1-1515)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 493 GTAGTGGTACTCTGTCCAAT 513

RESULT 15

US-10-311-453-30
; Sequence 30, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom 8
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-30

Alignment Scores:
Pred. No.: 504 Length: 1515
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-311-453-30 (1-1515)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 493 GTAGTGGTACTCTGTCCAAT 513

RESULT 16

US-10-817-483-26
; Sequence 26, Application US/10817483
; Publication No. US20040237147A1
; GENERAL INFORMATION:
; APPLICANT: Habben, Jeffrey E.
; APPLICANT: Zinselmeier, Christopher
; APPLICANT: Tomes, Dwight

APPLICANT: Abbitt, Shane
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Niu, Xiaomu
TITLE OF INVENTION: Modulation of Cytokinin Activity in
TITLE OF INVENTION: Plants
FILE REFERENCE: 0803R
CURRENT APPLICATION NUMBER: US/10/817,483
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: US 60/460,718
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 09/545,334
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 1560
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1560)
US-10-817-483-26

Alignment Scores:
Pred. No.: 519 Length: 1560
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-817-483-26 (1-1560)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 490 GTCGGTGGCACCTGTCTAAT 510

RESULT 17

US-10-817-483-30
Sequence 30, Application US/10817483
Publication No. US20040237147A1
GENERAL INFORMATION:
APPLICANT: Habben, Jeffrey E.
APPLICANT: Zinselmeier, Christopher
APPLICANT: Tomes, Dwight
APPLICANT: Abbitt, Shane
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Niu, Xiaomu
TITLE OF INVENTION: Modulation of Cytokinin Activity in
TITLE OF INVENTION: Plants
FILE REFERENCE: 0803R
CURRENT APPLICATION NUMBER: US/10/817,483
CURRENT FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: US 60/460,718
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 09/545,334
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1566
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1566)
US-10-817-483-30

Alignment Scores:

Pred. No.: 521 Length: 1566
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-817-483-30 (1-1566)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 469 GTGGGGGGCACGCTCTCCAAT 489

RESULT 18

US-10-014-101-27
Sequence 27, Application US/10014101
Publication No. US20030074698A1
GENERAL INFORMATION:
APPLICANT: Schmullling, Thomas
APPLICANT: Werner, Tom s
TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
TITLE OF INVENTION: physiology
FILE REFERENCE: 1195-2
CURRENT APPLICATION NUMBER: US/10/014,101
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: PCT/EP01/06833
PRIOR FILING DATE: 2001-06-16
PRIOR APPLICATION NUMBER: EP 00870132.8
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/258,415
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: EP 01870053.4
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 1572
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-014-101-27

Alignment Scores:

Pred. No.: 523 Length: 1572
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-014-101-27 (1-1572)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTCGGTGGGACGTTATCAAC 537

RESULT 19

US-10-326-184-9
Sequence 9, Application US/10326184
Publication No. US20030163847A1
GENERAL INFORMATION:
APPLICANT: Monsanto Company
TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
TITLE OF INVENTION: OXIDASE 1
FILE REFERENCE: MTC6781.1
CURRENT APPLICATION NUMBER: US/10/326,184
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/343,129
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1572
TYPE: DNA
US-10-014-101B-39 (1-7) x US-10-014-101-27 (1-1572)

; ORGANISM: Arabidopsis thaliana
US-10-326-184-9

Alignment Scores:
Pred. No.: 523 Length: 1572
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-326-184-9 (1-1572)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTCGGTGGACGTTATCAAAAC 537

RESULT 20

US-10-311-453-27
; Sequence 27, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-27

Alignment Scores:
Pred. No.: 523 Length: 1572
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-311-453-27 (1-1572)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTCGGTGGACGTTATCAAAAC 537

RESULT 21

US-09-938-842A-2089
; Sequence 2089, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2089
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2089

Alignment Scores:
Pred. No.: 524 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-938-842A-2089 (1-1575)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 535 GTCGGCGGACGTTGTCGAAC 555

RESULT 22

US-09-938-842A-2089
; Sequence 2089, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2089
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2089

Alignment Scores:
Pred. No.: 524 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-39 (1-7) x US-09-938-842A-2089 (1-1575)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 535 GTCGGCGGACGTTGTCGAAC 555

RESULT 23

US-10-014-101-28
; Sequence 28, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s

; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-28

Alignment Scores:
Pred. No.: 524 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-014-101-28 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTGCGAAC 555

RESULT 24
US-10-326-184-10
; Sequence 10, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-10

Alignment Scores:
Pred. No.: 524 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-326-184-10 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTGCGAAC 555

RESULT 25
US-10-326-184-11
; Sequence 11, Application US/10326184

; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-11

Alignment Scores:
Pred. No.: 524 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-326-184-11 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 502 GTGGGAGGTACGTTGTCAAAT 522

RESULT 26
US-10-311-453-28
; Sequence 28, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-28

Alignment Scores:
Pred. No.: 524 Length: 1575
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-311-453-28 (1-1575)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTGCGAAC 555

RESULT 27
US-10-326-184-11
; Sequence 11, Application US/10326184

```
US-10-437-963-88564
; Sequence 88564, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88564
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87402C.1
US-10-437-963-88564
Alignment Scores:
Pred. No.: 532 Length: 1599
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-437-963-88564 (1-1599)
QY 1 ValGlyGlyThrLeuSerAsn 7
| | | | | | | | | | | | | | | | | | | | | |
DB 502 GTAGGCGGACGCTGTCCAAC 522

RESULT 28
US-10-437-963-38170
; Sequence 38170, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 38170
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41832C.1
US-10-437-963-38170
Alignment Scores:
Pred. No.: 534 Length: 1605
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
```

```
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-437-963-38170 (1-1605)
QY 1 ValGlyGlyThrLeuSerAsn 7
| | | | | | | | | | | | | | | | | | | | | |
DB 517 GTGGGCGGCACCTCTCCAAC 537

RESULT 29
US-10-821-711-4
; Sequence 4, Application US/10821711
; Publication No. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Elysia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
US-10-821-711-4
Alignment Scores:
Pred. No.: 534 Length: 1605
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-821-711-4 (1-1605)
QY 1 ValGlyGlyThrLeuSerAsn 7
| | | | | | | | | | | | | | | | | | | | | |
DB 523 GTCGGCGGCACGCTGTCCAAC 543

RESULT 30
US-10-821-711-5
; Sequence 5, Application US/10821711
; Publication No. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Elysia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 5
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-10-821-711-5
Alignment Scores:
Pred. No.: 534 Length: 1605
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
```



```
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
US-10-014-101B-39 (1-7) x US-10-821-711-5 (1-1605)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 523 GTCGGCGGCACGCTGTCCAAC 543

RESULT 31
US-10-014-101-29
; Sequence 29, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-29

Alignment Scores:
Pred. No.: 536 Length: 1611
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-014-101B-39 (1-7) x US-10-014-101-29 (1-1611)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 499 GTTGAGGTACTCTCCAAT 519

RESULT 32
US-10-311-453-29
; Sequence 29, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 1611
```

```
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-29

Alignment Scores:
Pred. No.: 536 Length: 1611
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-10-014-101B-39 (1-7) x US-10-311-453-29 (1-1611)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 499 GTTGAGGTACTCTCCAAT 519

RESULT 33
US-10-817-483-28
; Sequence 28, Application US/10817483
; Publication No. US20040237147A1
; GENERAL INFORMATION:
; APPLICANT: Habben, Jeffrey E.
; APPLICANT: Zinselmeier, Christopher
; APPLICANT: Tomes, Dwight
; APPLICANT: Abbott, Shane
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Niu, Xiaomu
; TITLE OF INVENTION: Modulation of Cytokinin Activity in
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 0803R
; CURRENT APPLICATION NUMBER: US/10/817,483
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/460,718
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 09/545,334
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1617)
US-10-817-483-28

Alignment Scores:
Pred. No.: 538 Length: 1617
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
US-10-014-101B-39 (1-7) x US-10-817-483-28 (1-1617)

QY 1 ValGlyGlyThrLeuSerAsn 7
Db 517 GTCGGCGGCACGCTCTCCAAC 537

RESULT 34
US-10-014-101-34
; Sequence 34, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
```

; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-34

Alignment Scores:
Pred. No.: 539 Length: 1620
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-014-101-34 (1-1620)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 508 GTTGGAGGTACACTCTCCAAT 528

RESULT 35

US-10-311-453-34
; Sequence 34, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-34

Alignment Scores:
Pred. No.: 539 Length: 1620
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-311-453-34 (1-1620)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 508 GTTGGAGGTACACTCTCCAAT 528

RESULT 36

US-10-326-184-12
; Sequence 12, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-12

Alignment Scores:
Pred. No.: 540 Length: 1623
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-326-184-12 (1-1623)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 511 GTTGGAGGTACACTCTCCAAT 531

RESULT 37

US-10-817-483-32
; Sequence 32, Application US/10817483
; Publication No. US20040237147A1
; GENERAL INFORMATION:
; APPLICANT: Habben, Jeffrey E.
; APPLICANT: Zinselmeier, Christopher
; APPLICANT: Tones, Dwight
; APPLICANT: Abbott, Shane
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Niu, Xiaomu
; TITLE OF INVENTION: Modulation of Cytokinin Activity in
; FILE REFERENCE: 0803R
; CURRENT APPLICATION NUMBER: US/10/817,483
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/460,718
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 09/545,334
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1629)
US-10-817-483-32

Alignment Scores:
Pred. No.: 542 Length: 1629
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-817-483-32 (1-1629)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 502 GTCGGCGGACGCTGTCCAAT 522

RESULT 38
US-10-326-184-20
; Sequence 20, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-10-326-184-20

Alignment Scores:
Pred. No.: 551 Length: 1655
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-326-184-20 (1-1655)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 535 GTCGGCGGACGTTGTCCAAC 555

RESULT 39
US-10-437-963-70571
; Sequence 70571, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 70571
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7112C.1

US-10-437-963-70571

Alignment Scores:

Pred. No.: 556 Length: 1670
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-437-963-70571 (1-1670)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 603 GTTGGAGGCACACTGTCCAAT 623

RESULT 40
US-10-437-963-83827
; Sequence 83827, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 83827
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83121C.1

US-10-437-963-83827

Alignment Scores:
Pred. No.: 557 Length: 1673
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-39 (1-7) x US-10-437-963-83827 (1-1673)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 609 GTCGGTGGCACGCTCTCCAAC 629

Search completed: February 18, 2005, 10:12:20
Job time : 333.98 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 02:20:24 ; Search time 825.44 Seconds
(without alignments)
322.797 Million cell updates/sec

Title: US-10-014-101B-39
Perfect score: 35
Sequence: 1 VGGTILSN 7

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2 1/USPTO.spool/US10014101/runat 16022005 075846 7952/app query.fasta 1.796
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101 @CGN 1 1 5453 @runat 16022005 075846 7952 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	116	9 CG802105	CG802105 1118027F1
2	35	100.0	162	9 BX890851	BX890851 Arabidops
3	35	100.0	230	8 BZ643095	BZ643095 OGAOF23TC
4	35	100.0	299	9 CR490530	CR490530 Medicago
5	35	100.0	306	1 AV424619	AV424619 AV424619
6	35	100.0	307	8 CC131284	CC131284 NDL.32E23
7	35	100.0	309	5 BX476387	BX476387 DKFZp686N
8	35	100.0	362	8 BZ622937	BZ622937 ig81e07.b
9	35	100.0	399	9 CE648629	CE648629 tigr-gss-

C	10	35	100.0	445	6	CD703115	CD703115 EST19706
	11	35	100.0	451	5	BQ588342	BQ588342 E012308-0
	12	35	100.0	461	1	AU289504	AU289504 AU289504
C	13	35	100.0	470	8	AQ795075	AQ795075 nbxb0055C
	14	35	100.0	473	1	AU243228	AU243228 AU243228
	15	35	100.0	476	4	BI930687	BI930687 EST550576
	16	35	100.0	481	4	BM137409	BM137409 WHE0463-0
	17	35	100.0	485	9	CG927858	CG927858 MBEII59TR
	18	35	100.0	487	5	BP031101	BP031101 BP031101
C	19	35	100.0	491	9	CR399680	CR399680 Arabidops
	20	35	100.0	504	9	CC656142	CC656142 OGUDB93TH
C	21	35	100.0	506	8	AQ827482	AQ827482 HS_5304.A
C	22	35	100.0	511	6	CB640717	CB640717 OSJNEal6A
C	23	35	100.0	515	5	BQ869165	BQ869165 QGD5F19.Y
C	24	35	100.0	518	5	BX283649	BX283649 BX283649
C	25	35	100.0	520	7	CR775437	CR775437 DKFZp469C
	26	35	100.0	525	4	BI498566	BI498566 sai15g12.
C	27	35	100.0	536	8	AQ510474	AQ510474 nbxb0095B
	28	35	100.0	540	2	AW224503	AW224503 EST302946
	29	35	100.0	542	7	CF603749	CF603749 BACCA01.0
	30	35	100.0	550	9	CNS000MU	AL083412 Arabidops
	31	35	100.0	551	9	CG357974	CG357974 OGZBG58TV
C	32	35	100.0	556	7	CV057457	CV057457 BNEL28a6
	33	35	100.0	559	4	BI700658	BI700658 sai27e03.
	34	35	100.0	564	2	AW736360	AW736360 EST332279
C	35	35	100.0	564	8	CC022210	CC022210 3591.1.28
	36	35	100.0	566	5	BU084470	BU084470 ear19h02.
C	37	35	100.0	567	9	CL157422	CL157422 104.345.1
C	38	35	100.0	571	8	BZ706895	BZ706895 OGBBD30TC
	39	35	100.0	573	7	CO600263	CO600263 DG8-199k1
C	40	35	100.0	574	5	BP133582	BP133582 BP133582
	41	35	100.0	576	8	BZ949154	BZ949154 CH240.37E
C	42	35	100.0	583	7	CV057888	CV057888 BNEL31h8
	43	35	100.0	584	4	BG130984	BG130984 EST463876
	44	35	100.0	584	8	BZ333618	BZ333618 hx71d05.g
	45	35	100.0	585	2	BF648633	BF648633 NF048D04E

ALIGNMENTS

RESULT 1
CG802105 1118027F12.Y1 1118 - RescueMu Grid S Zea may's genomic, genomic
LOCUS survey sequence.
DEFINITION CG802105 116 bp DNA linear GSS 10-NOV-2003
ACCESSION CG802105.1 GI:38237891
VERSION GSS.
KEYWORDS Zea may's
SOURCE Zea may's
ORGANISM Zea may's
REFERENCE 1 (bases 1 to 116)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 1118027 row: 47
Class: transposon-tagged.
Location/Qualifiers
1. .116
/organism="Zea may's"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Alignment Scores:
Pred. No.: 225 Length: 116
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x CG802105 (1-116)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||
Db 61 GTCGGCGGCACACTGTCCAAC 81

RESULT 2

BX890851

LOCUS BX890851 162 bp DNA linear GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-157A04-013241,
genomic survey sequence.

ACCESSION BX890851

VERSION BX890851.1 GI:39923346

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.

TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147

PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weissshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE

AUTHORS Li, Y., Strizhov, N., Rosso, M.G. and Weissshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer

COMMENT Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g56970. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

Location/Qualifiers
1..162
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-157A04-013241"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Alignment Scores:
Pred. No.: 321 Length: 162
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x BX890851 (1-162)

QY 1 ValGlyGlyThrLeuSerAsn 7

|||
Db 71 GTCGGTGGGACGTATCAAC 91

RESULT 3

BZ643095/c

LOCUS BZ643095 230 bp DNA linear GSS 29-JAN-2003

DEFINITION OGAF23TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0107C22,
genomic survey sequence.

ACCESSION BZ643095

VERSION BZ643095.1 GI:28104206

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

TITLE Consortium for Maize Genomics

JOURNAL Unpublished (2002)

COMMENT Other_GSSs: OGAF23TM

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1..230

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0107C22"
/clone_lib="ZM_0.7.1.5_KB"
/note="Vector: pBC5K-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Alignment Scores:
Pred. No.: 465 Length: 230
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x BZ643095 (1-230)

Qy 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 80 GTCGGCGGCACGCTGTCCAAC 60

RESULT 4

CR490530/c

LOCUS

CR490530 299 bp DNA linear GSS 11-JUN-2004
Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
truncatula, genomic survey sequence.

ACCESSION

CR490530

VERSION

CR490530.1 GI:48652106

KEYWORDS

GSS.

SOURCE

Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 299)

Genoscope.

Direct Submission

Submitted (10-JUN-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Location/Qualifiers

1. .299

/organism="Medicago truncatula"

/mol_type="genomic DNA"

/cultivar="Jemalong A17"

/db_xref="taxon:3880"

/clone_lib="MTH2"

/note="Vector: pBelobAC11 ; Site_1: HindIII ; Site_2:

HindIII ; Cook, D.R. and Kim, D.J-Genoscope sequence ID :

mth2-161F3FM1"

ORIGIN

Alignment Scores:

Pred. No.: 613 Length: 299

Score: 35.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x CR490530 (1-299)

Qy 1 ValGlyGlyThrLeuSerAsn 7

|||||

Db 42 GTTGAGGCACTCTTTCGAAT 22

RESULT 5

AV424619

LOCUS

AV424619 306 bp mRNA linear EST 10-MAR-2004
corniculatus var. japonicus young plants (two-week old) Lotus
corniculatus var. japonicus cDNA clone MWM042d03_r 5', mRNA

sequence.
AV424619
AV424619.1 GI:7781717
EST.

ORGANISM

Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

1 (bases 1 to 306)

AUTHORS

Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.

Generation of 7137 non-redundant expressed sequence tags from a

legume, Lotus japonicus

DNA Res. 7 (2), 127-130 (2000)

20277479

10819328

Contact: Yasukazu Nakamura

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers

1. .306

/organism="Lotus corniculatus var. japonicus"

/mol_type="mRNA"

/isolate="Miyakojima MG-20"

/db_xref="taxon:34305"

/clone="MWM042d03_r"

/tissue_type="whole plant"

/dev_stage="two-week old plant"

/clone_lib="Lotus japonicus young plants (two-week old)"

/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:

XhoI; synonym: Lotus japonicus"

ORIGIN

Alignment Scores:

Pred. No.: 629 Length: 306

Score: 35.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-014-101B-39 (1-7) x AV424619 (1-306)

Qy 1 ValGlyGlyThrLeuSerAsn 7

|||||

Db 173 GTGGAGGCGACGTTATCTAAC 193

RESULT 6

CC131284/c

LOCUS

CC131284

DEFINITION

NDL.32E23.T7 Notre Dame Liverpool Aedes aegypti genomic clone

NDL.32E23, genomic survey sequence.

CC131284.1 GI:30000339

CC131284

GSS.

Aedes aegypti (yellow fever mosquito)

Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;

Stegomyia.

1 (bases 1 to 307)

Loftus,B., Shetty,J., Knudson,D. and Severson,D.

BAC end sequencing of Aedes aegypti

Unpublished (2003)

Other_GSSs: NDL.32E23.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

```

Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.

FEATURES
    source
        Location/Qualifiers
            1..307
                /organism="Aedes aegypti"
                /mol_type="genomic DNA"
                /strain="Liverpool"
                /db_xref="taxon:7159"
                /clone="NDL.32E23"
                /clone_lib="Notre Dame Liverpool"
                /note="Vector: pECBAC1; Site_1: Hind III; The library was
                prepared from whole body tissue of newly hatched L1 larvae
                by David Severson at the University of Notre Dame and
                Hongbin Zhang"

ORIGIN
Alignment Scores:
Pred. No.:      631      Length:      307
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     100.00%  Indels:      0
DB:              8      Gaps:          0

US-10-014-101B-39 (1-7) x CC131284 (1-307)

QY      1 ValGlyGlyThrLeuSerAsn 7
Db      98 GTCGGTGTACTGTCCAAC 78

RESULT 7
BX476387/c
LOCUS   BX476387      309 bp      mRNA      linear      EST 04-SEP-2003
DEFINITION   DKFZp686N06185_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION   BX476387
VERSION     BX476387.1  GI:31673644
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 309)
AUTHORS    Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
            EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
            Unpublished (2003)
            Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone (DKFZp686N06185) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
    source
        Location/Qualifiers
            1..309
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKFZp686N06185"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="686 (synonym: hlcc3)"
                /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
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ORIGIN
CDNA-collection"
Alignment Scores:
Pred. No.:      635      Length:      309
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     100.00%  Indels:      0
DB:              5      Gaps:          0

US-10-014-101B-39 (1-7) x BX476387 (1-309)

QY      1 ValGlyGlyThrLeuSerAsn 7
Db      108 GTGGCGGAACGCTTCTTAAT 88

RESULT 8
BZ622937/c
LOCUS   BZ622937      362 bp      DNA      linear      GSS 16-JAN-2003
DEFINITION   ig81e07.b1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ACCESSION   BZ622937
VERSION     BZ622937.1  GI:27774789
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1  (bases 1 to 362)
            Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N.,
            Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
            Zutavern,T., McCombie,W.R. and Martienssen,R.A.
            Genomic shotgun sequences from Zea mays (methyl-filtered)
            Unpublished (2002)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mcombie@cshl.org
            Plate: ig81 row: e Column: 07
            Seq primer: -21M13UnivFwd
            Class: shotgun
            High quality sequence stop: 362.
            Location/Qualifiers
                1..362
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ig81e07"
                    /lab_host="DH5a"
                    /clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
                    /note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
                    The vector was digested with XbaI and one nucleotide was
                    added by fill in in the recessive 3' end. The genomic DNA
                    was nebulized, end repaired, adaptor ligated and size
                    fractionated using sephadex. The resulting fragments were
                    between 0.8 and 3 kb and were cloned into the vector (.x/y
                    reads in M13mp19, .b/g reads in pUC19). The same ligation
                    was transformed into DH5a."

FEATURES
    source
        Location/Qualifiers
            1..362
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="B73"
                /db_xref="taxon:4577"
                /clone="ig81e07"
                /lab_host="DH5a"
                /clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
                /note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
                The vector was digested with XbaI and one nucleotide was
                added by fill in in the recessive 3' end. The genomic DNA
                was nebulized, end repaired, adaptor ligated and size
                fractionated using sephadex. The resulting fragments were
                between 0.8 and 3 kb and were cloned into the vector (.x/y
                reads in M13mp19, .b/g reads in pUC19). The same ligation
                was transformed into DH5a."

ORIGIN
Alignment Scores:
Pred. No.:      751      Length:      362
Score:          35.00    Matches:      7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     100.00%  Indels:      0
DB:              8      Gaps:          0
```

US-10-014-101B-39 (1-7) x BZ6222937 (1-362)

Qy 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 136 GTCGGCGGCAGCGCTCTCCAAC 116

RESULT 9

CE648629

LOCUS

DEFINITION tigr-gss-dog-17000367296724 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION

CE648629

VERSION

CE648629.1 GI:36967469

KEYWORDS

GSS.

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 399)

Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,

Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and

Venter,J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

PUBMED

14512627

CONTACT: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1. .399

/organism="Canis familiaris"

/mol_type="genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from

peripheral blood"

ORGANISM

Alignment Scores:

Pred. No.: 833

Score: 35.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 9

Length: 399

Matches: 7

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-10-014-101B-39 (1-7) x CE648629 (1-399)

Qy 1 ValGlyGlyThrLeuSerAsn 7

|||||

Db 127 GTTGAGGAGACCTTTCCAAC 147

RESULT 10

CD703115/c

LOCUS

DEFINITION CD703115 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD703115
VERSION CD703115.1 GI:32233809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 445)

Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and

TITLE

JOURNAL

COMMENT

Zeng,Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

Contact: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn.

Location/Qualifiers

1. .445

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA

library from southern Chinese"

ORIGIN

Alignment Scores:

Pred. No.: 935

Score: 35.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Length: 445

Matches: 7

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-10-014-101B-39 (1-7) x CD703115 (1-445)

Qy 1 ValGlyGlyThrLeuSerAsn 7

|||||

Db 111 GTGGCGGACGCTTTCTAAT 91

RESULT 11

BQ588342

LOCUS

DEFINITION

BQ588342

E012308-024-008-P04-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

024-008-P04 5-PRIME, mRNA sequence.

ACCESSION

BQ588342

VERSION

BQ588342.1 GI:26117925

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 451)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED

12472698

CONTACT: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 451

Std Error: 0.00

Plate: 8 row: P column: 04

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

1. .451

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:184499"

/db_xref="taxon:161934"
/clone="024-008-P04"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 948 Length: 451
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-39 (1-7) x BQ588342 (1-451)

QY 1 ValGlyGlyThrLeuSerAsn 7

Db 152 GTGGTGGTACGTTGTCTAAT 172

RESULT 12

AU289504

LOCUS

DEFINITION AU289504 zinnia cultured mesophyll cell equalized cDNA Zinnia
elegans cDNA clone Z4008, mRNA sequence.

ACCESSION AU289504

VERSION AU289504.1 GI:24249624

KEYWORDS EST.

SOURCE Zinnia elegans

ORGANISM

Zinnia elegans
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Zinnia.

REFERENCE

AUTHORS

1 (bases 1 to 461)
Demura,T., Tashiro,G., Horiguchi,G., Kishimoto,N., Kubo,M.,
Matsuoka,N., Minami,A., Nagata-Hiwatashi,M., Nakamura,K.,
Okamura,Y., Sassa,N., Suzuki,S., Yazaki,J., Kikuchi,S. and
Fukuda,H.

TITLE
Visualization by comprehensive microarray analysis of gene
expression programs during transdifferentiation of mesophyll cells
into xylem cells

JOURNAL

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
Contact: Taku Demura

Morphogenesis Research Group

RIKEN Plant Science Center

1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9605

Fax: 81-45-503-9573

Email: demura@postman.riken.go.jp

This clone was obtained at our laboratory.

Seq primer: M13 forward.

FEATURES

source

Location/Qualifiers

1..461

/organism="Zinnia elegans"

/mol_type="mRNA"

/cultivar="Canary bird"

/db_xref="taxon:34245"

/clone="Z4008"

/tissue_type="mesophyll cell"

/clone_lib="zinnia cultured mesophyll cell equalized cDNA"

/note="Vector: pGEM-T easy; cultured in tracheary element

ORIGIN

differentiation-inductive medium"

Alignment Scores:

Pred. No.: 970 Length: 461
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-39 (1-7) x AU289504 (1-461)

QY 1 ValGlyGlyThrLeuSerAsn 7

Db 384 GTAGTGGTACTTTGTCTAAC 404

RESULT 13

AQ795075/c

LOCUS

DEFINITION AQ795075 470 bp DNA linear GSS 04-AUG-1999
nbxb0055C05r CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0055C05r, genomic survey
sequence.

ACCESSION AQ795075

VERSION AQ795075.1 GI:5703544

KEYWORDS GSS.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 470)

Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: GGAAACAGCTATGACCATG

Class: BAC ends

High quality sequence stop: 319.

FEATURES

source

Location/Qualifiers

1..470

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="nbxb0055C05r"

/tissue_type="Leaf"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice BAC Library"

/note="Vector: pBelobAC11; Site 1: HindIII; Site 2:

HindIII; Rice is one of two most popular grains in the

world. Half of the world population especially those

inhabiting highly populated areas of the humid tropics

and subtropics, rely on rice as their primary source of

carbohydrate. Monocotyledonous rice is a diploid plant

(2n=24) with a haploid genome equivalent of 431 Mbp

(Arumuganathan and Earle, 1991). The relatively small

genome of rice, three times larger than that of

Arabidopsis, makes it suitable for genomic studies. In

order to facilitate positional cloning, physical mapping

and genome sequencing of rice, we have constructed a BAC

library from Oryza sativa, Nipponbare variety. The

library contains 36,864 clones with an average insert size

of 128.5 Kb providing 10.9 haploid genome equivalents. The

deep coverage allows the isolation a particular sequence

with a probability of 99.9 %. Two high density filters,

each containing 18,432 clones (doubly spotted), represent

the whole library for colony screening."

ORIGIN

Alignment Scores:
Pred. No.: 991 Length: 470
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x AQ795075 (1-470)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 417 GTTGGAGGCACACTGTGCAAT 397

RESULT 14

AU243228

LOCUS AU243228 Medaka eye cDNA library (SNK01) Oryzias latipes cDNA clone
DEFINITION NGY29.03f, mRNA sequence.

ACCESSION AU243228

VERSION AU243228.1 GI:18155807

KEYWORDS EST.

SOURCE Oryzias latipes (Japanese medaka)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE

AUTHORS Sanaka,E., Hori,H., Naruse,K., Mitani,H. and Tanaka,M.

TITLE Medaka EST analysis

JOURNAL Unpublished (2001)

COMMENT Contact: Emi Sanaka

Department of Biological Sciences

Graduate School of Science, Nagoya University

Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan

Tel: 81-52-789-2973

Fax: 81-52-789-2974

Email: sanaka@bio.nagoya-u.ac.jp

This clone was isolated from Medaka eye cDNA library (SNK01) 5'end.

FEATURES

source

Location/Qualifiers

1..473

/organism="Oryzias latipes"

/mol_type="mRNA"

/strain="wild type"

/db_xref="taxon:8090"

/clone="NGY29.03f"

/tissue_type="eye"

/dev_stage="adult"

/clone_lib="Medaka eye cDNA library (SNK01)"

/note="Wild samples from Okayama Pref.(Southern part of

Japan)"

ORIGIN

Alignment Scores:

Pred. No.: 997 Length: 473
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-39 (1-7) x AU243228 (1-473)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 446 GTTGGGGGACACTTAGCAAT 466

RESULT 15

BI930687

LOCUS BI930687 476 bp mRNA linear EST 18-OCT-2001
DEFINITION EST550576 tomato flower, 8 mm to preanthesis buds Lycopersicon
esculentum cDNA clone CTC17F5 5' end, mRNA sequence.

ACCESSION BI930687

VERSION BI930687.1 GI:16245159

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 476)

AUTHORS

van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

Generation of ESTs from tomato flower tissue, buds 8 mm -

preanthesis

Unpublished (2001)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics

Institute

Seq primer: T3.

Location/Qualifiers

1..476

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CTC17F5"

/tissue_type="flower"

/dev_stage="buds 8mm to preanthesis"

/clone_lib="tomato flower, 8 mm to preanthesis buds"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; supplier: Cornell University; sequencing: The

Institute for Genomic Research; Flower buds and flowers

were taken from greenhouse plants (4-8 wks old, TA496).

They were immediately frozen in liquid nitrogen and then

size-separated while remaining frozen."

ORIGIN

Alignment Scores:

Pred. No.: 1e+03 Length: 476
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x BI930687 (1-476)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 281 GTCGGAGGTACTCTGTCTAAT 301

RESULT 16

BM137409

LOCUS BM137409 481 bp mRNA linear EST 28-NOV-2001
DEFINITION WHE0463-0466_K01_K01ZS Wheat Fusarium graminearum infected spike
cDNA library_Triticum aestivum cDNA clone WHE0463-0466_K01_K01,
mRNA sequence.

ACCESSION BM137409

VERSION BM137409.1 GI:17146176

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 481)

AUTHORS Anderson,O.D., Chao,S., Han,P.S., Heinen,S., Hsia,C.C., Kang,Y., Kruger,W.M., Iazo,G.R., Miller,S., Muehlbauer,G.J., Miller,R., Pritsch,C., Rausch,C.J., Seaton,C.L., Tong,J.C., Vance,C. and Wilson,C.F.

TITLE The structure and function of the expressed portion of the wheat genomes - Fusarium graminearum infected spike cDNA library

JOURNAL Unpublished (2001)

COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST could be of wheat or fungal origin.
Seq primer: Stratagene SK primer.

FEATURES
source
Location/Qualifiers
1. .481
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/clone="WHE0463-0466_K01_K01"
/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/clone_lib="Wheat Fusarium graminearum infected spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Spikes were sprayed at anthesis with Fusarium graminearum. Total RNA, and poly(A) RNA were prepared and pooled from infected spike at 0, 6, 12, 24, 36 and 48 hours after inoculation, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in G. Muehlbauer lab at the University of Minnesota (Kruger, W.M., Muehlbauer, G.J., Pritsch, C., Vance, C.). The cDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN
Alignment Scores:
Pred. No.: 1.02e+03 Length: 481
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-39 (1-7) x BM137409 (1-481)
Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 205 GTGGGCGGACCCCTCTCCAAC 225
RESULT 17
CG927858
LOCUS CG927858 485 bp DNA linear GSS 12-DEC-2003
DEFINITION MBEII59TR mth2 Medicago truncatula genomic clone 62I21, genomic survey sequence.
ACCESSION CG927858
VERSION CG927858.1 GI:39788945
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

REFERENCE
AUTHORS Medicago.
TITLE 1 (bases 1 to 485)
JOURNAL Town,C.D., Shetty,J., Koo,H. and Feldblyum,T.F.
COMMENT Sequencing of BAC ends from Medicago truncatula Unpublished (2003)
Other GSSs: MBEII59TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: CAGGAACAGCTATGACC
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1. .485
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="62I21"
/clone_lib="mth2"
/note="Vector: pBelOBAC11; Site 1: HindIII; Site 2: HindIII; Cook, D.R. and Kim, D.J, unpublished"

ORIGIN
Alignment Scores:
Pred. No.: 1.02e+03 Length: 485
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-39 (1-7) x CG927858 (1-485)
Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 397 GTTGGTGACACTCTCTCTAAT 417
RESULT 18
BP031101
LOCUS BP031101 487 bp mRNA linear EST 19-AUG-2004
DEFINITION BP031101 Lotus corniculatus var. japonicus flower Lotus corniculatus var. japonicus cDNA clone MF053g01_f 3', mRNA sequence.

ACCESSION BP031101
VERSION BP031101.1 GI:45408261
KEYWORDS EST.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
REFERENCE 1 (bases 1 to 487)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Characteristics of the Lotus japonicus Gene Repertoire Deduced from Large-Scale Expressed Sequence Tag (EST) Analysis
JOURNAL Plant Mol. Biol. 54 (3), 405-414 (2004)
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
source
Location/Qualifiers
1. .487
/organism="Lotus corniculatus var. japonicus"
/mol_type="mRNA"
/isolate="Miyakojima MG-20"
/db_xref="taxon:34305"
/clone="MF053g01_f"
/tissue_type="flower"

```
ORIGIN
/clone_lib="Lotus corniculatus var. japonicus flower"

Alignment Scores:
Pred. No.: 1.03e+03 Length: 487
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-39 (1-7) x BP031101 (1-487)
LOCUS CR399680 491 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-820D08-025640, genomic survey sequence.
ACCESSION CR399680
VERSION CR399680.1 GI:46940408
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weissshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weissshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 491)
AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weissshaar,B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At2g19500.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .491
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-820D08-025640"
```

```
ORIGIN
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC106 (GenBank accession number: AJ537513). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Alignment Scores:
Pred. No.: 1.04e+03 Length: 491
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x CR399680 (1-491)
QY 1 ValGlyGlyThrLeuSerAsn 7
Db 397 GTCGGAGGAGCTCTTCCAAT 377

RESULT 20
CC656142 504 bp DNA linear GSS 19-JUN-2003
LOCUS OGUDB93TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0412P18,
DEFINITION genomic survey sequence.
ACCESSION CC656142
VERSION CC656142.1 GI:32059361
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 504)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUDB93TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .504
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0412P18"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 1.07e+03 Length: 504
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```


US-10-014-101B-39 (1-7) x CC656142 (1-504)

Qy 1 ValGlyGlyThrLeuSerAsn 7
| | | | | | | | | | | | | | | | | |
Db 280 GTCGGCGGACGCTGTCCAAT 300

RESULT 21

AQ827482/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AQ827482 506 bp DNA linear GSS 27-AUG-1999
HS_5304_A1_C02_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=880 Col=3 Row=E, genomic survey sequence.
AQ827482
AQ827482.1 GI:5793544
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 506)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 880 row: E column: 3
Seq primer: T7
Class: BAC ends
High quality sequence stop: 506.

FEATURES

source

1. .506

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=880 Col=3 Row=E"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:

Pred. No.: 1.07e+03 Length: 506
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x AQ827482 (1-506)

Qy 1 ValGlyGlyThrLeuSerAsn 7
| | | | | | | | | | | | | | | | | |

Db 367 GTAGGAGGTACTCTCTCCAAC 347

RESULT 22

CB640717/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CB640717 511 bp mRNA linear EST 08-APR-2003
OSJNEa16A24.f OSJNEa Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEa16A24 5', mRNA sequence.
CB640717
CB640717.1 GI:29635708
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 511)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: atc agc ggc cgc gat cc
BACKWARD: aat taa ccc tca cta aag gg
Plate: 16 row: A column: 24
Seq primer: atc agc ggc cgc gat cc.
Location/Qualifiers

FEATURES

source

1. .511

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEa16A24"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEa"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice_Blast (Che
86061)"

ORIGIN

Alignment Scores:

Pred. No.: 1.08e+03 Length: 511
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-39 (1-7) x CB640717 (1-511)

Qy 1 ValGlyGlyThrLeuSerAsn 7
| | | | | | | | | | | | | | | | | |

Db 481 GTTGAGGCACACTGTCCAAT 461

RESULT 23

BQ869165/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BQ869165 515 bp mRNA linear EST 14-AUG-2002
QGDSF19.YG.ab1 QG_ABCDI lettuce salinas lactuca sativa cDNA clone
QGDSF19, mRNA sequence.
BQ869165
BQ869165.1 GI:22254922
EST.
Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
1 (bases 1 to 515)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmil.ucdavis.edu]
belongs to contig QG_CA_Contig6961, see <http://cgpdb.ucdavis.edu/> for details.
Plate: QGD5 row: F column: 19.

FEATURES
source

1. .515
Location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGD5P19"
/lab_host="E.coli"
/clone_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRCNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpdb.ucdavis.edu/>
TAG_TISSUE=flowers pre-fertilized
TAG_LIB=QG ABCDI lettuce salinas
TAG_SEQ=GCTTGACGGG"

ORIGIN

Alignment Scores:
Pred. No.: 1.09e+03 Length: 515
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-39 (1-7) x BQ869165 (1-515)

Qy 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 401 GTCGGCGGAACGCTGTCTAAC 381

RESULT 24
BX283649/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BX283649
BX283649 NIH MGC 21 Homo sapiens cDNA clone IMAGE3956474, mRNA sequence.
IMAGE:3956474, mRNA sequence.
BX283649
BX283649.1 GI:28848103
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.

TITLE
JOURNAL
COMMENT

Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp958K03832.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
pCMV-M13u, Primer sequence: CGTTGTAAACGACGCCAGT.

FEATURES
source

1. .518
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp958K03832 ; IMAGE:3956474"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
Pred. No.: 1.1e+03 Length: 518
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-39 (1-7) x BX283649 (1-518)

Qy 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 85 GTGGCGGAACGCTTTCTAAT 65

RESULT 25
CR775437/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CR775437
DKF2p469C0965_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKF2p469C0965 5', mRNA sequence.
CR775437
CR775437.1 GI:52618686
EST.
Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 520)
Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469C0965
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES

source
1. .520
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469C0965"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:
Pred. No.: 1.1e+03 Length: 520
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-39 (1-7) x CR775437 (1-520)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 129 GTGGGCGGAACGCTTCTAAT 109

RESULT 26

BI498566

LOCUS

DEFINITION
sai15912.y1 Gm-c1053 Glycine max cdna clone GENOME SYSTEMS CLONE
ID: Gm-c1053-3407 5' similar to TR:O22213 T32G6.3 PROTEIN.
/, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 391.

Location/Qualifiers

source

1. .525
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Harosoy"

/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1053-3407"
/tissue_type="Whole seedling, 3 week old, greenhouse
grown"
/lab_host="DH10B"
/clone_lib="Gm-c1053"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cdna library was
constructed from mRNA isolated from whole seedlings of 3
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cdna fragments followed by XhoI digestion. The cdna
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cdna fragments were transformed into DH10B host cells
(GibcoBRL). This library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
University."

ORIGIN

Alignment Scores:
Pred. No.: 1.1e+03 Length: 525
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x BI498566 (1-525)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 133 GTGGGCGGAACCTCTCGAAC 153

RESULT 27

AQ510474/C

LOCUS

DEFINITION

AQ510474 536 bp DNA linear GSS 04-MAY-1999
nbxb0095B17f CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0095B17f, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence stop: 346.

Location/Qualifiers

FEATURES

source

1. .536
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0095B17f"

/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
/note="Vector: pBelosAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."

ORIGIN

Alignment Scores:
Pred. No.: 1.14e+03 Length: 536
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x AQ510474 (1-536)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 417 GTTGAGGCACACTGTGGAAT 397

RESULT 28

AW224503

LOCUS

DEFINITION
AW224503 540 bp mRNA linear EST 18-MAY-2001
EST302946 tomato root, plants pre-anthesis, Cornell University
Lycopersicon esculentum cDNA clone cLEY1A15 similar to Zea mays
cytokinin oxidase, mRNA sequence.

ACCESSION

VERSION

AW224503.1 GI:6536187

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE

AUTHORS

van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
Tanksley,S.D.

Generation of ESTs from tomato root tissue

Unpublished (1999)

COMMENT

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

source

1. .540

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="cLEY1A15"

/tissue_type="root"

/dev_stage="plants in pre-anthesis stage"
/clone_lib="tomato root, plants pre-anthesis, Cornell
University"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
(USDA-ARS, Ithaca, NY 14850)."

ORIGIN

Alignment Scores:
Pred. No.: 1.15e+03 Length: 540
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-39 (1-7) x AW224503 (1-540)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 180 GTCGAGGTACTCTGTCTAAT 200

RESULT 29

CF603749

LOCUS

DEFINITION
BACCA01_001055 Grape Berry pSPORT1 Library Vitis vinifera cDNA 5',
mRNA sequence.

ACCESSION

CF603749

VERSION

CF603749.1 GI:37184395

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS

1 (bases 1 to 542)
Moser,C., Segala,C., Fontana,P., Salakhudtinov,I., Gatto,P.,
Pindo,M., Zyprian,E., Toepfer,R., Grando,M.S. and Velasco,R.

Expressed sequence tags from different organs of Vitis vinifera

Unpublished (2003)

Contact: Moser C

Laboratorio di Genetica Molecolare

Istituto Agrario di San Michele all'Adige (IASMA)

via E. Mach 1, San Michele all'Adige (TN), I-38010, Italia

Tel: 0039-0461-615314

Fax: 0039-0461-650956

Email: claudio.moser@ismaa.it

The sequencing work has been funded by the 'Fondazione Cassa di

Risparmio di Trento e Rovereto'

High quality sequence stop: 542.

FEATURES

source

i. .542

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Pinot Noir"

/db_xref="taxon:29760"

/sex="Hermaphrodite"

/dev_stage="veraison"

/lab_host="DH10B"

/clone_lib="Grape Berry pSPORT1 Library"

/note="Organ: berry; Vector: pSPORT1; Site_1: NotI;
Site_2: Sali"

ORIGIN

Alignment Scores:
Pred. No.: 1.15e+03 Length: 542
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-39 (1-7) x CF603749 (1-542)

(days post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Barley EST endosperm library"
/note="Vector: Ziplox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the barley cultivar Himalaya. cDNA was synthesised from pooled 10, 12, and 15 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of Ziplox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

ORIGIN

Alignment Scores:
Pred. No.: 1.18e+03 Length: 556
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-39 (1-7) x CV057457 (1-556)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 512 GTCGGCGGCACGCTCTCCAAC 492

RESULT 33

BI700658
LOCUS sai27e03.y1 Gm-c1053 Glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION ID: Gm-c1053-4445 5' similar to TR:022213 T32G6.3 PROTEIN.
/, mRNA sequence.

ACCESSION BI700658
VERSION BI700658.1 GI:15663287
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 559)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE

JOURNAL Public Soybean EST Project
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 433.

Location/Qualifiers

1. .559
source /organism="Glycine max"
/mol_type="mRNA"
/cultivar="Harosoy"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1053-4445"
/tissue_type="Whole seedling, 3 week old, greenhouse grown"

/lab_host="DH10B"
/clone_lib="Gm-c1053"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

ORIGIN

Alignment Scores:
Pred. No.: 1.19e+03 Length: 559
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-39 (1-7) x BI700658 (1-559)

Qy 1 ValGlyGlyThrLeuSerAsn 7
Db 166 GTCGGCGGCACGCTCTCCAAT 186

RESULT 34

AW736360
LOCUS AW736360
DEFINITION EST332279 KV3 Medicago truncatula cDNA clone PKV3-12E18, mRNA
sequence.

ACCESSION AW736360
VERSION AW736360.1 GI:7643143
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE

1 (bases 1 to 564)
AUTHORS VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.

ESTs from roots of Medicago truncatula after Rhizobium inoculation

TITLE

JOURNAL Unpublished (1999)
COMMENT Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvanden@cbs.umn.edu
Texas A&M EST name:T255800e
TIGR sequence name:MTEAF33TK
More information is available at...

'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA GAA CTA gtg gat CC).
Location/Qualifiers
1. .564
source /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-12E18"

FEATURES

source

/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XL0LR"
/clone_lib="KV3"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

ORIGIN

Alignment Scores:
Pred. No.: 1.2e+03 Length: 564
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-39 (1-7) x AW736360 (1-564)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 538 GTTGGTGGAACTCTCTCTAAT 558

RESULT 35

CC022210/c

LOCUS

DEFINITION

3591_1_28_1_G02.y_1 3591 - RescueMu Grid P Zea mays genomic,

genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 564)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3591.1 28.1 row: 15

Class: transposon-tagged.

Location/Qualifiers

1. .564

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="3591 - RescueMu Grid P"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site_1: BamHI; Site_2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid P was grown at Molokai in 2002. DNA was

extracted from leaf strips, double digested using BamHI

.ORIGIN

Alignment Scores:
Pred. No.: 1.2e+03 Length: 564
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x CC022210 (1-564)

Qy 1 ValGlyGlyThrLeuSerAsn 7

Db 325 GTCGGTGGCACCTTGCTAAT 305

RESULT 36

BU084470

LOCUS

DEFINITION

sarl9h02.y1 Gm-c1049 Glycine max cDNA clone SOYBEAN CLONE ID:

Gm-c1049-7252 5', similar to TR:Q9SU77 Q9SU77 CYTOKININ OXIDASE-LIKE

PROTEIN. ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 566)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,

Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,

Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,

Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,

Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,

McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is

available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco

High quality sequence stop: 421.

Location/Qualifiers

1. .566

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Clark"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1049-7252"

/tissue_type="whole seedlings of greenhouse grown plants"

/dev_stage="3 week old"

/lab_host="DH10B"

/clone_lib="Gm-c1049"

/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:

XhoI; The Clark NIL was constructed and seed was provided

by Dr. J. Specht, University of Nebraska (Shoemaker and

Specht, 1995). The cDNA library was constructed from mRNA

isolated from whole seedlings of 3 week old greenhouse

grown plants. Complementary DNA was synthesized from mRNA

and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

FEATURES

source

using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

ORIGIN

Alignment Scores:
Pred. No.: 1.21e+03 Length: 566
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-39 (1-7) x BU084470 (1-566)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 133 GTGGAGGGACACTTTCAT 153

RESULT 37

CL157422/c

LOCUS

DEFINITION 104 345 10783550 114 31477 110 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10783550, genomic survey sequence.

ACCESSION

CL157422

VERSION CL157422.1 GI:40659037

KEYWORDS

GSS.

SOURCE

Sorghum bicolor (sorghum)

ORGANISM

Sorghum bicolor

REFERENCE

AUTHORS

Budiman,M.A., Flick,E., Jones,J., Nunberg,A., Citek,R.W., Robbins,D., Rohlfling,T., Bradford,K., Fries,J., McMenamy,J., Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.

TITLE

Genethresher methylation filtered genomic sequences from Sorghum bicolor

JOURNAL

COMMENT

Unpublished (2004)

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: 345 row: e column: 14

Seq primer: M13/pUC Forward

Class: shotgun

High quality sequence stop: 567.

FEATURES

source

Location/Qualifiers

1..567

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="10783550"

/clone_lib="Sorghum methylation-filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."

ORIGIN

Alignment Scores:

Pred. No.: 1.21e+03 Length: 567
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-39 (1-7) x CL157422 (1-567)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 451 GTGGCGGGACGCTGTGGAAC 431

RESULT 38

BZ706895/c

LOCUS

DEFINITION BZ706895 571 bp DNA linear GSS 19-FEB-2003 OGBBD30TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0123E12, genomic survey sequence.

ACCESSION

BZ706895

VERSION BZ706895.1 GI:28426936

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 571)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfling,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: sheared ends.

FEATURES

source

Location/Qualifiers

1..571

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBMA0123E12"

/clone_lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.: 1.22e+03 Length: 571
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-39 (1-7) x BZ706895 (1-571)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||

Db 23 GTCGGTGGCACCTTGCTAAT 3

RESULT 39

CO600263

LOCUS

DEFINITION DG8-199k19 DG8-testis Canis familiaris cDNA 3', mRNA sequence. EST 21-JUL-2004

ACCESSION

CO600263

VERSION

CO600263.1 GI:50445827

KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 573)
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J., and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.

FEATURES
source
1..573
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG8-testis"
/note="Organ: testis; Vector: Dog pBluescript LION"

ORIGIN

Alignment Scores:
Pred. No.: 1.22e+03 Length: 573
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-39 (1-7) x CO600263 (1-573)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 359 GTGGGAGGTACGTTAAGTAAT 379

RESULT 40
BP133582/c
LOCUS BP133582 574 bp mRNA linear EST 16-JUL-2003
DEFINITION BP133582 MAT001 Nicotiana tabacum cDNA clone BY5863, mRNA sequence.
ACCESSION BP133582
VERSION BP133582.1 GI:32876467
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 574)
AUTHORS Matsuoka, K., Tashiro, G., Horiguchi, T., Demura, T. and Fukuda, H.
TITLE Profiling growth-phase dependent gene expression of tobacco BY-2
cells by comprehensive microarray analysis
JOURNAL Unpublished (2003)
COMMENT Contact: Ken Matsuoka
Morphogenesis Research Group
RIKEN Plant Science Center
1-7-2 Suehirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
Email: by2@psc.riken.go.jp, URL: http://mrg.psc.riken.go.jp/strc/
The cDNA library was constructed from mRNA isolated from lag (9 h),
log (72 h) and stationary (7 days) old BY-2 cells.

FEATURES
source
1..574
/organism="Nicotiana tabacum"
/mol_type="mRNA"

/cultivar="Bright Yellow No.2"
/db_xref="taxon:4097"
/clone="BY5863"
/cell_line="BY-2"
/clone_lib="MAT001"
/note="Vector: pGEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"

ORIGIN

Alignment Scores:
Pred. No.: 1.22e+03 Length: 574
Score: 35.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-39 (1-7) x BP133582 (1-574)

QY 1 ValGlyGlyThrLeuSerAsn 7
|||||
Db 272 GTTGAGGGACTTTGTCCAAT 252

Search completed: February 18, 2005, 07:00:50
Job time : 832.44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2005, 21:59:48 ; Search time 1234.08 Seconds
(without alignments)
353.378 Million cell updates/sec

Title: US-10-014-101B-40
Perfect score: 50
Sequence: 1 VLGGGLQFPC 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2 1/USPTO spool/US10014101/runat 16022005 075845 7936/app_query.fasta_1.796
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101 @CGN 1 1 2886 @runat 16022005 075845 7936 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	50	100.0	5817	9 HSM807454	BX647310 Homo sapi
2	50	100.0	261203	2 AC126952	AC126952 Rattus no
3	48	96.0	196806	10 AC027184	AC027184 Mus muscu
4	48	96.0	197646	10 AC136376	AC136376 Mus muscu

5	48	96.0	255818	2 AC084055	AC084055 Mus muscu
C 6	46	92.0	155214	10 AL627406	AL627406 Mouse DNA
C 7	46	92.0	212540	2 AC102912	AC102912 Mus muscu
C 8	45	90.0	168177	2 AC023914	AC023914 Homo sapi
C 9	45	90.0	192682	10 AC107769	AC107769 Mus muscu
10	45	90.0	196902	2 AC105345	AC105345 Homo sapi
11	45	90.0	200000	2 AC007104	AC007104 Homo sapi
12	45	90.0	214284	9 AC116643	AC116643 Homo sapi
C 13	45	90.0	217225	10 AL513345	AL513345 Mouse DNA
14	45	90.0	236274	10 AC119853	AC119853 Mus muscu
C 15	45	90.0	277408	2 AC124136	AC124136 Mus muscu
C 16	44	88.0	1509	6 E07190	E07190 DNA encodin
17	44	88.0	68743	9 AL139349	AL139349 Human DNA
18	44	88.0	163410	9 AC006198	AC006198 Homo sapi
19	44	88.0	177725	2 AC105162	AC105162 Mus muscu
20	44	88.0	196529	10 AC102630	AC102630 Mus muscu
C 21	44	88.0	232605	1 AE017222	AE017222 Thermus t
C 22	44	88.0	279448	8 AY661656	AY661656 Sorghum b
C 23	43	86.0	5183	6 AR042369	AR042369 Sequence
C 24	43	86.0	5183	6 AR052277	AR052277 Sequence
C 25	43	86.0	5868	6 AR241188	AR241188 Sequence
C 26	43	86.0	5868	6 AR262645	AR262645 Sequence
27	43	86.0	6113	6 AX346724	AX346724 Sequence
C 28	43	86.0	6177	6 CQ715456	CQ715456 Sequence
C 29	43	86.0	6188	9 HUMHOXY1	D45132 Homo sapien
30	43	86.0	6436	6 AX345583	AX345583 Sequence
C 31	43	86.0	6704	6 AX780015	AX780015 Sequence
32	43	86.0	7603	6 AX281287	AX281287 Sequence
33	43	86.0	7603	6 AX345210	AX345210 Sequence
C 34	43	86.0	7942	9 HSU17838	U17838 Homo sapien
35	43	86.0	9504	6 AX323793	AX323793 Sequence
C 36	43	86.0	55622	2 AC023042	AC023042 Homo sapi
37	43	86.0	59433	2 AC091556	AC091556 Homo sapi
38	43	86.0	76891	2 AC011925	AC011925 Homo sapi
39	43	86.0	110000	2 AC020850_3	Continuation (4 of
40	43	86.0	132446	2 AC024999	AC024999 Homo sapi
41	43	86.0	138054	2 AC146325	AC146325 Felis cat
42	43	86.0	151188	9 HS1177E19	AL031277 Human DNA
C 43	43	86.0	165527	10 AL592403	AL592403 Mouse DNA
C 44	43	86.0	170336	10 AC125137	AC125137 Mus muscu
45	43	86.0	172793	2 AC023659	AC023659 Homo sapi

ALIGNMENTS

RESULT 1	HSM807454/c	HSM807454	5817 bp	mRNA	linear	PRI 30-AUG-2003
LOCUS	Homo sapiens mRNA; cDNA DKFZp686D2193 (from clone DKFZp686D2193).					
DEFINITION						
ACCESSION	BX647310					
VERSION	BX647310.1	GI:34366338				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 5817)					
AUTHORS	Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.					
CONSRM	The German Human cDNA Consortium					
TITLE	Direct Submission					
JOURNAL	Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764					
COMMENT	Neuherberg, GERMANY					
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer					
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;					
	sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing					
	consortium of the German Genome Project.					
	This clone (DKFZp686D2193) is available at the RZPD in Berlin.					
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059					
	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further					
	information about the clone and the sequencing project is available					
	at http://mips.gsf.de/proj/cDNA/.					
FEATURES	Location/Qualifiers					

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source
1. .5817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686D2193"
/tissue_type="human retina"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
polyA_signal 5781. .5786
polyA_site 5792
ORIGIN
Alignment Scores:
Pred. No.:      21.1      Length:      5817
Score:          50.00     Matches:      9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%     Indels:      0
DB:              9          Gaps:      0

US-10-014-101B-40 (1-9) x HSM807454 (1-5817)

QY      1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db      1227 GTTCTGGTGGCTGGCCAGTTCTGC 1201

RESULT 2
AC126952
LOCUS
DEFINITION
Rattus norvegicus clone CH230-1514, *** SEQUENCING IN PROGRESS ***,
8 unordered pieces.
AC126952
AC126952.5 GI:305222508
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 261203)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuheva,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokeleneh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
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Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 261203)
Worley,K.C.
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 261203)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25009166.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GGQA
Center clone name: CH230-1514
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 194451 bases at least Q40
Consensus quality: 199590 bases at least Q30
Consensus quality: 203294 bases at least Q20
Estimated insert size: 203856; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 250096: contig of 250096 bp in length
* 250097 250196: gap of unknown length
* 250197 251466: contig of 1270 bp in length
```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

* 251467 251566: gap of unknown length
* 251567 252675: contig of 1109 bp in length
* 252676 252775: gap of unknown length
* 252776 253837: contig of 1062 bp in length
* 253838 253937: gap of unknown length
* 253938 255287: contig of 1350 bp in length
* 255288 255387: gap of unknown length
* 255388 257029: contig of 1642 bp in length
* 257030 257129: gap of unknown length
* 257130 259608: contig of 2479 bp in length
* 259609 259708: gap of unknown length
* 259709 261203: contig of 1495 bp in length.

FEATURES

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/db_xref="taxon:10116"
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85376. .86946
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139057. .139631
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misc_feature
misc_feature

ORIGIN

Alignment Scores:
Pred. No.: 706 Length: 261203
Score: 50.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC126952 (1-261203)

QY 1 ValLeuGlyLeuGlyGlnPheCys 9

Db 108136 GTTCTGGGTGGACTAGGTCAATTTTGT 108162

RESULT 3

AC027184
LOCUS AC027184 196806 bp DNA linear ROD 17-SEP-2004
DEFINITION Mus musculus chromosome 14, clone RP23-138C14, complete sequence.
AC027184
ACCESSION AC027184.15 GI:52219300
VERSION
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 196806)

REFERENCE

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Mus musculus chromosome 14, clone RP23-138C14

JOURNAL

REFERENCE 2 (bases 1 to 196806)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczký,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 196806)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (12-AUG-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 196806)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (17-SEP-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 17, 2004 this sequence version replaced gi:51172695.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence submissions@broad.mit.edu

----- Project Information

Center project name: L7288

Center clone name: 138_C14

FEATURES

source

Location/Qualifiers

1. .196806


```
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="14"
/map="14"
/clone="RP23-138C14"
/clone_lib="RPCI-23 Female Mouse BAC"
complement(2884..2984)
/rpt_family="PB1D7"
3639..3730
/rpt_family="PB1D7"
3757..3943
/rpt_family="B2_Mm2"
complement(4007..5580)
/rpt_family="L1_MM"
5645..5732
/rpt_family="MMAR1"
5733..5878
/rpt_family="B1_MM"
5879..6717
/rpt_family="MMAR1"
6732..6871
/rpt_family="MMAR1"
complement(6847..6981)
/rpt_family="B1_MM"
7038..7175
/rpt_family="B1_MM"
complement(7963..8147)
/rpt_family="B3"
complement(8193..8278)
/rpt_family="PB1D7"
complement(8280..8397)
/rpt_family="B1F"
complement(8398..8423)
/rpt_family="ID_B1"
8460..8551
/rpt_family="(TG)n"
complement(8552..8697)
/rpt_family="B1_MM"
8698..8721
/rpt_family="(TG)n"
8722..8791
/rpt_family="(TG)n"
8933..8954
/rpt_family="AT_rich"
complement(9117..9162)
/rpt_family="B4A"
complement(9163..9279)
/rpt_family="PB1D7"
10158..10226
/rpt_family="L2"
complement(10219..10305)
/rpt_family="L2"
11284..11388
/rpt_family="PB1D10"
12016..12406
/rpt_family="L2"
complement(12407..12553)
/rpt_family="B1_MM"
12554..12631
/rpt_family="L2"
complement(12919..13123)
/rpt_family="ORR1D"
complement(13124..13471)
/rpt_family="RLTR10"
complement(13472..13527)
/rpt_family="ORR1D"
13720..13914
/rpt_family="B3"
13930..14055
/rpt_family="B1_MM"
14386..14567
/rpt_family="ID_B1"
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repeat_region      14878..14974
                    /rpt_family="L2"
repeat_region      complement(15018..15378)
                    /rpt_family="MTD"
repeat_region      15379..15591
                    /rpt_family="L2"
repeat_region      16811..16892
                    /rpt_family="PB1D9"
repeat_region      complement(16893..17288)
                    /rpt_family="MTC"
repeat_region      17641..17809
                    /rpt_family="B3"
                    17890..17907
unsure             /note="single clone coverage"
                    17893..17901
unsure             /note="<30 qual single clone coverage"
repeat_region      17905..17936
                    /rpt_family="(CCCCCA)n"
unsure             17918..17924
                    /note="<30 qual SNGL region"
repeat_region      complement(18176..18331)
repeat_region      /rpt_family="MT2C"
                    complement(18310..18508)
repeat_region      /rpt_family="MT2A"
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Alignment Scores:

Pred. No.:	1.34e+03	Length:	196806
Score:	48.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	10	Gaps:	0

US-10-014-101B-40 (1-9) x AC027184 (1-196806)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 23543 GTCATGGGTGGACTTGGTCAGTCTCTGT 23569

RESULT 4

AC136376

LOCUS

AC136376 Mus musculus chromosome 14 clone RP23-243M12, complete sequence.

DEFINITION

AC136376

AC136376.3 GI:50839084

VERSION

HTG.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 197646)

Wilson,R.K.

The sequence of Mus musculus clone

Unpublished

2 (bases 1 to 197646)

McPherson,J.D. and Waterston,R.H.

Direct Submission

Submitted (31-OCT-2002) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 197646)

Wilson,R.K.

Direct Submission

Submitted (28-MAY-2004) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 197646)

Wilson,R.K.

Direct Submission

Submitted (30-JUL-2004) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

On Jul 30, 2004 this sequence version replaced gi:47777615.

COMMENT

Center: Washington University Genome Sequencing Center

Center code: WUGSC
Web site: <http://genome.wustl.edu>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0243M12

FEATURES
source
1. 197646
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="14"
/clone="RP23-243M12"

ORIGIN

Alignment Scores:
Pred. No.: 1.34e+03 Length: 197646
Score: 48.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 96.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x AC136376 (1-197646)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
||||:|||||||
Db 173706 GTCATGGGTGGACTGGTCAGTTCTGT 173732

RESULT 5
AC084055 255818 bp DNA linear HTG 08-JUN-2002
LOCUS Mus musculus chromosome 2 clone RP23-359C19 strain C57BL6/J,
DEFINITION WORKING DRAFT SEQUENCE, 37 unordered pieces.

ACCESSION AC084055
VERSION AC084055.6 GI:21358695
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 255818)
Montgomery,K.T., Grills,G., Han,J., Chiu,D., Decker,J., Fusina,M.,
Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J.,
Perera,A.M., Shim,C., Thomas,E.C. and Kucherlapati,R.

TITLE High Throughput Mouse Sequencing
JOURNAL Unpublished

REFERENCE
AUTHORS 2 (bases 1 to 255818)
Montgomery,K.T., Grills,G., Han,J., Chiu,D., Decker,J., Fusina,M.,
Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J.,
Perera,A., Shim,C., Thomas,E. and Kucherlapati,R.

TITLE Direct Submission
JOURNAL Submitted (12-OCT-2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA

REFERENCE
AUTHORS 3 (bases 1 to 255818)
Montgomery,K.T., Grills,G., Han,J., Chiu,D., Decker,J., Fusina,M.,
Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J.,
Perera,A., Shim,C., Thomas,E. and Kucherlapati,R.

TITLE Direct Submission
JOURNAL Submitted (08-JUN-2002) Harvard Partners Center for Genetics and
Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
02139, USA

COMMENT On Jun 8, 2002 this sequence version replaced gi:21306620.

-----Genome Center
Center: Harvard Partners Genome Center
Center Code: HPGC
Web site: <http://www.hpcgg.org/Sequence/mouse.html>
Contact: hpgc@medel.mgh.harvard.edu
-----Summary Statistics-----
Center project name: AEK
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%

*Consensus quality: 238808 at least Q20
*Consensus quality: 233351 at least Q30
*Consensus quality: 226354 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 255098 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 6.8 x in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 69107: contig of 69107 bp in length
* 69108 69127: gap of unknown length
* 69128 122703: contig of 53576 bp in length
* 122704 122723: gap of unknown length
* 122724 149769: contig of 27046 bp in length
* 149770 149789: gap of unknown length
* 149790 165917: contig of 16128 bp in length
* 165918 165937: gap of unknown length
* 165938 177120: contig of 11183 bp in length
* 177121 177140: gap of unknown length
* 177141 186790: contig of 9650 bp in length
* 186791 186810: gap of unknown length
* 186811 195013: contig of 8203 bp in length
* 195014 195033: gap of unknown length
* 195034 201988: contig of 6955 bp in length
* 201989 202008: gap of unknown length
* 202009 206594: contig of 4586 bp in length
* 206595 206614: gap of unknown length
* 206615 209494: contig of 2880 bp in length
* 209495 209514: gap of unknown length
* 209515 210395: contig of 881 bp in length
* 210396 210415: gap of unknown length
* 210416 211816: contig of 1401 bp in length
* 211817 211836: gap of unknown length
* 211837 213977: contig of 2141 bp in length
* 213978 213997: gap of unknown length
* 213998 216349: contig of 2352 bp in length
* 216350 216369: gap of unknown length
* 216370 218294: contig of 1925 bp in length
* 218295 218314: gap of unknown length
* 218315 220170: contig of 1856 bp in length
* 220171 220190: gap of unknown length
* 220191 223017: contig of 2827 bp in length
* 223018 223037: gap of unknown length
* 223038 226049: contig of 3012 bp in length
* 226050 226069: gap of unknown length
* 226070 227531: contig of 1462 bp in length
* 227532 227551: gap of unknown length
* 227552 230223: contig of 2672 bp in length
* 230224 230243: gap of unknown length
* 230244 232298: contig of 2055 bp in length
* 232299 232318: gap of unknown length
* 232319 233599: contig of 1281 bp in length
* 233600 233619: gap of unknown length
* 233620 236005: contig of 2386 bp in length
* 236006 236025: gap of unknown length
* 236026 236902: contig of 877 bp in length
* 236903 236922: gap of unknown length
* 236923 238851: contig of 1929 bp in length
* 238852 238871: gap of unknown length
* 238872 240684: contig of 1813 bp in length
* 240685 240704: gap of unknown length
* 240705 242179: contig of 1475 bp in length
* 242180 242199: gap of unknown length
* 242200 243272: contig of 1073 bp in length
* 243273 243292: gap of unknown length
* 243293 244114: contig of 822 bp in length

* 244115 244134: gap of unknown length
* 244135 246257: contig of 2123 bp in length
* 246258 246277: gap of unknown length
* 246278 248050: contig of 1773 bp in length
* 248051 248070: gap of unknown length
* 248071 248889: contig of 819 bp in length
* 248890 248909: gap of unknown length
* 248910 250641: contig of 1732 bp in length
* 250642 250661: gap of unknown length
* 250662 252029: contig of 1368 bp in length
* 252030 252049: gap of unknown length
* 252050 253649: contig of 1600 bp in length
* 253650 253669: gap of unknown length
* 253670 254711: contig of 1042 bp in length
* 254712 254731: gap of unknown length
* 254732 255818: contig of 1087 bp in length.
* 254732 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL6/J"
 /db_xref="taxon:10090"
 /chromosome="2"
 /clone="RP23-359C19"
 /sex="male"
 1. .69107
 /note="assembly_name:Contig124"
69128. .122703
/note="assembly_name:Contig123"
122724. .149769
/note="assembly_name:Contig122
clone end:SP6
vector_side:right"
149790. .165917
/note="assembly_name:Contig121"
165938. .177120
/note="assembly_name:Contig120"
177141. .186790
/note="assembly_name:Contig119"
186811. .195013
/note="assembly_name:Contig118"
195034. .201988
/note="assembly_name:Contig117"
202009. .206594
/note="assembly_name:Contig116"
206615. .209494
/note="assembly_name:Contig115"
209515. .210395
/note="assembly_name:Contig114"
210416. .211816
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211837. .213977
/note="assembly_name:Contig112"
213998. .216349
/note="assembly_name:Contig111"
216370. .218294
/note="assembly_name:Contig110"
218315. .220170
/note="assembly_name:Contig109"
220191. .223017
/note="assembly_name:Contig108"
223038. .226049
/note="assembly_name:Contig107"
226070. .227531
/note="assembly_name:Contig106"
227552. .230223
/note="assembly_name:Contig105"
230244. .232298
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232319. .233599
/note="assembly_name:Contig103"
233620. .236005
/note="assembly_name:Contig102"

FEATURES

source

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/note="assembly_name:Contig101"
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/note="assembly_name:Contig100"
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/note="assembly_name:Contig99"
misc_feature 240705. .242179
/note="assembly_name:Contig98"
misc_feature 242200. .243272
/note="assembly_name:Contig97"
misc_feature 243293. .244114
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Alignment Scores:
Pred. No.: 1.7e+03 Length: 255818
Score: 48.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 96.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC084055 (1-255818)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
||||:|||||||
Db 76857 GTCATGGGTGGACTTGGTCAGTCTGT 76883

RESULT 6
AL627406/c
LOCUS AL627406 155214 bp DNA linear ROD 09-JUL-2002
DEFINITION Mouse DNA sequence from clone RP23-188A12 on chromosome 4, complete
sequence.
ACCESSION AL627406
VERSION AL627406.15 GI:21727347
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 155214)
AUTHORS Tracey,A.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 10, 2002 this sequence version replaced gi:21711854.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-188A12 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>

/note="assembly_fragment"
128683..212540
/note="assembly_fragment"

misc_feature
ORIGIN

Alignment Scores:
Pred. No.: 3.52e+03 Length: 212540
Score: 46.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 92.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC102912 (1-212540)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 122307 GTTTGGTGGCTCGGTAGGTTCTGT 122281

RESULT 8
AC023914/c 168177 bp DNA linear HTG 20-SEP-2000
LOCUS
DEFINITION Homo sapiens clone RP11-44K20, WORKING DRAFT SEQUENCE, 22 unordered
pieces.
AC023914 GI:10198362
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168177)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-44K20
Unpublished
2 (bases 1 to 168177)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bada,F., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.

Direct Submission
Submitted (20-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 20, 2000 this sequence version replaced gi:9102875.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1087
Center clone name: 44 K 20
----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157528 bases at least Q40
Consensus quality: 162841 bases at least Q30
Consensus quality: 164870 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 166077; sum-of-contigs
Quality coverage: 4.3 in Q20 bases; agarose-fp
Quality coverage: 4.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved:

1 1263: contig of 1263 bp in length
1264 1363: gap of 100 bp
1364 2399: contig of 1036 bp in length
2400 2499: gap of 100 bp
2500 3713: contig of 1214 bp in length
3714 3813: gap of 100 bp
3814 27125: contig of 23312 bp in length
27126 27225: gap of 100 bp
27226 28854: contig of 1629 bp in length
28855 28954: gap of 100 bp
28955 31625: contig of 2671 bp in length
31626 31725: gap of 100 bp
31726 34084: contig of 2359 bp in length
34085 34184: gap of 100 bp
34185 36582: contig of 2398 bp in length
36583 36682: gap of 100 bp
36683 39629: contig of 2947 bp in length
39630 39729: gap of 100 bp
39730 43900: contig of 4171 bp in length
43901 44000: gap of 100 bp
44001 46837: contig of 2837 bp in length
46838 46937: gap of 100 bp
46938 52599: contig of 5662 bp in length
52600 52699: gap of 100 bp
52700 60235: contig of 7536 bp in length
60236 60335: gap of 100 bp
60336 67600: contig of 7265 bp in length
67601 67700: gap of 100 bp
67701 76219: contig of 8519 bp in length
76220 76319: gap of 100 bp
76320 85003: contig of 8684 bp in length
85004 85103: gap of 100 bp
85104 95875: contig of 10772 bp in length
95876 95975: gap of 100 bp
95976 108080: contig of 12105 bp in length
108081 108180: gap of 100 bp
108181 126996: contig of 18816 bp in length
126997 127096: gap of 100 bp
127097 145024: contig of 17928 bp in length
145025 145124: gap of 100 bp
145125 166554: contig of 21430 bp in length
166555 166654: gap of 100 bp
166655 168177: contig of 1523 bp in length.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-44K20"
/clone_lib="RPCI-11 Human Male BAC"
1..1263
/note="assembly_fragment
clone end:SP6
vector_side:left"
misc_feature
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ORIGIN

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Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 2 Gaps: 0
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US-10-014-101B-40 (1-9) x AC023914 (1-168177)

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QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 24360 GTGTTGGGGGGCTTGGTAGCTTCG 24334
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RESULT 9

AC107769/c AC107769 192682 bp DNA linear ROD 30-SEP-2003

LOCUS Mus musculus chromosome 16, clone RP23-130N20, complete sequence.

DEFINITION AC107769

ACCESSION AC107769

VERSION AC107769.7 GI:33342391

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 192682)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE
JOURNAL
REFERENCE
AUTHORS

Mus musculus chromosome 16, clone RP23-130N20

Unpublished

2 (bases 1 to 192682)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 192682)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (04-JUL-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 192682)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
JOURNAL Submitted (30-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 5 (bases 1 to 192682)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 30, 2003 this sequence version replaced gi:32451548.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20430
Center clone name: 130_N_20

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Pred. No.: 5.04e+03 Length: 192682
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x AC107769 (1-192682)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 20391 GTGTTAGGGGTTGGGGGATTTTTGT 20365

RESULT 10

AC105345

LOCUS

DEFINITION Homo sapiens BAC clone RP11-689P11 from 4, complete sequence.

ACCESSION AC105345

VERSION AC105345.3 GI:21686936

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM: Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 196902)

AUTHORS Sulston,J.E. and Waterston,R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

196902 bp DNA linear PRI 03-JUL-2002

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PUBMED	9847074	repeat_region	/rpt_family="MER1_type"
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AUTHORS	Du,H., Haglund,K. and Spalding,L.	repeat_region	/rpt_family="MER1_type"
TITLE	The sequence of Homo sapiens BAC clone RP11-689P11	repeat_region	13054. .13410
JOURNAL	Unpublished (2001)	repeat_region	/rpt_family="L1"
REFERENCE	3 (bases 1 to 196902)	repeat_region	14877. .14987
AUTHORS	Waterston,R.H.	repeat_region	/rpt_family="MIR"
TITLE	Direct Submission	repeat_region	15657. .15956
JOURNAL	Submitted (31-DEC-2001) Genome Sequencing Center, Washington	repeat_region	/rpt_family="Alu"
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	MO 63108, USA	repeat_region	/rpt_family="L2"
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AUTHORS	Waterston,R.H.	repeat_region	/rpt_family="L1"
TITLE	Direct Submission	repeat_region	20364. .20502
JOURNAL	Submitted (06-MAR-2002) Genome Sequencing Center, Washington	repeat_region	/rpt_family="L2"
	University School of Medicine, 4444 Forest Park Parkway, St. Louis,	repeat_region	23610. .23744
	MO 63108, USA	repeat_region	/rpt_family="L2"
REFERENCE	5 (bases 1 to 196902)	repeat_region	24921. .25224
AUTHORS	Waterston,R.	repeat_region	/rpt_family="Alu"
TITLE	Direct Submission	repeat_region	27502. .28052
JOURNAL	Submitted (03-JUL-2002) Department of Genetics, Washington	repeat_region	/rpt_family="MER2_type"
	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	repeat_region	28053. .28267
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Alignment Scores:
Pred. No.: 5.14e+03 Length: 196902
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-40 (1-9) x AC105345 (1-196902)

Qy 1 ValLeuGlyLeuGlyGlnPheCys 9
Db 97321 GTGTTGGGGGGCTTGGTAGCTTCTGC 97347

RESULT 11
AC007104
LOCUS AC007104 200000 bp DNA linear HTG 17-JUL-1999
DEFINITION Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 16
unordered pieces.
AC007104
VERSION AC007104.4 GI:5523795
KEYWORDS HTG; HTGS PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 200000)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 200000)

AUTHORS
TITLE
JOURNAL

COMMENT

Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
Direct Submission
Submitted (17-MAR-1999) Department of Genetics, Stanford Human
Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
On Jul 17, 1999 this sequence version replaced gi:4757683.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1369: contig of 1369 bp in length
* 1370 3774: gap of unknown length
* 3775 4878: contig of 1104 bp in length
* 4879 7283: gap of unknown length
* 7284 8555: contig of 1272 bp in length
* 8556 10960: gap of unknown length
* 10961 12207: contig of 1247 bp in length
* 12208 14612: gap of unknown length
* 14613 16262: contig of 1650 bp in length
* 16263 18667: gap of unknown length
* 18668 20176: contig of 1509 bp in length
* 20177 22581: gap of unknown length
* 22582 24278: contig of 1697 bp in length
* 24279 26683: gap of unknown length
* 26684 28198: contig of 1515 bp in length
* 28199 30603: gap of unknown length
* 30604 32359: contig of 1756 bp in length
* 32360 34764: gap of unknown length
* 34765 39958: contig of 5194 bp in length
* 39959 42363: gap of unknown length
* 42364 57085: contig of 14722 bp in length
* 57086 59490: gap of unknown length
* 59491 74905: contig of 15415 bp in length
* 74906 77310: gap of unknown length
* 77311 84273: contig of 6963 bp in length
* 84274 86678: gap of unknown length
* 86679 118061: contig of 31383 bp in length
* 118062 120466: gap of unknown length
* 120467 152965: contig of 32499 bp in length
* 152966 155370: gap of unknown length
* 155371 200000: contig of 44630 bp in length.

FEATURES
source
1..200000
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"

ORIGIN

Alignment Scores:
Pred. No.: 5.22e+03 Length: 200000
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC007104 (1-200000)

Qy 1 ValLeuGlyLeuGlyGlnPheCys 9
Db 137654 GTGTTGGGGGGCTTGGTAGCTTCTGC 137680

RESULT 12
AC116643
LOCUS AC116643
DEFINITION Homo sapiens BAC clone RP11-637J21 from 4, complete sequence.
AC116643
ACCESSION AC116643
VERSION AC116643.11 GI:28173293
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 214284)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 214284)
AUTHORS Du, F. and Haglund, K.
TITLE The sequence of Homo sapiens BAC clone RP11-637J21
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 214284)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 214284)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 214284)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 214284)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 31, 2003 this sequence version replaced gi:27753869.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0637J21

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong

and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6
NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Discrepant bases between AC007104 and clone sequence.
Data from AC105345 and AC007104 was used to finish this clone.

FEATURES	Location/Qualifiers
source	1..214284
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="4"
	/map="4"
	/clone="RP11-637J21"
	/clone_lib="RPCI-11"
repeat_region	207..514
	/rpt_family="Alu"
repeat_region	515..622
	/rpt_family="L2"
repeat_region	709..927
	/rpt_family="L2"
repeat_region	952..1046
	/rpt_family="L2"
repeat_region	1311..1741
	/rpt_family="ERV1"
repeat_region	1746..2055
	/rpt_family="Alu"
repeat_region	2734..2862
	/rpt_family="MIR"
repeat_region	3899..4199
	/rpt_family="Alu"
repeat_region	5071..5180
	/rpt_family="MIR"
repeat_region	5330..5678
	/rpt_family="MaLR"
repeat_region	5867..6558
	/rpt_family="L1"
repeat_region	6635..6946
	/rpt_family="Alu"
repeat_region	6963..7046
	/rpt_family="L1"
repeat_region	7114..7194
	/rpt_family="MIR"
repeat_region	7188..7297
	/rpt_family="L2"
repeat_region	7851..7927
	/rpt_family="MIR"
repeat_region	7928..7958
	/rpt_family="(TGAA)n"
repeat_region	8945..9131
	/rpt_family="MIR"
repeat_region	9216..9330
	/rpt_family="L2"
repeat_region	9367..9532
	/rpt_family="L1"
repeat_region	9533..9850
	/rpt_family="Alu"
repeat_region	10243..10351
	/rpt_family="MER1_type"
repeat_region	11570..11679
	/rpt_family="MIR"
repeat_region	12216..12453
	/rpt_family="L1"
repeat_region	12454..12587
	/rpt_family="Alu"
repeat_region	12792..12947
	/rpt_family="L1"
repeat_region	12958..13341
	/rpt_family="L1"
repeat_region	13355..13659

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repeat_region /rpt_family="Alu"
13660. .13793
repeat_region /rpt_family="Alu"
13794. .14175
repeat_region /rpt_family="L1"
14176. .14531
repeat_region /rpt_family="MaLR"
14532. .15069
repeat_region /rpt_family="L1"
15070. .15202
repeat_region /rpt_family="Alu"
15203. .15491
repeat_region /rpt_family="Alu"
15492. .15514
repeat_region /rpt_family="Alu"
15515. .16246
repeat_region /rpt_family="L1"
16249. .16578
repeat_region /rpt_family="Alu"
16598. .16657
repeat_region /rpt_family="L1"
16658. .16984
repeat_region /rpt_family="Alu"
16985. .17354
repeat_region /rpt_family="L1"
17365. .17435
repeat_region /rpt_family="Alu"
17436. .17782
repeat_region /rpt_family="ERV1"
17784. .17974
repeat_region /rpt_family="MaLR"
18131. .18439
repeat_region /rpt_family="Alu"
18779. .19085
repeat_region /rpt_family="Alu"
19432. .19542
repeat_region /rpt_family="Tip100"
19543. .20119
repeat_region /rpt_family="ERV1"
20120. .20505
repeat_region /rpt_family="MaLR"
20506. .20748
repeat_region /rpt_family="ERV1"
20779. .20884
repeat_region /rpt_family="Tip100"
20889. .21097
repeat_region /rpt_family="Tip100"
21359. .21466
repeat_region /rpt_family="L2"

Alignment Scores:
Pred. No.: 5.56e+03 Length: 214284
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-40 (1-9) x AC116643 (1-214284)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 34363 GTGTTGGGGGGCTTGGTAGCTTCTGC 34389

RESULT 13
AL513345/c 217225 bp DNA linear ROD 17-NOV-2001
LOCUS Mouse DNA sequence from clone RP23-129N7 on chromosome 15, complete
DEFINITION sequence.
ACCESSION AL513345
VERSION AL513345.20 GI:17017730
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
```

```
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 217225)
AUTHORS Dunn,M.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Nov 20, 2001 this sequence version replaced gi:15722124.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep RP23-129N7 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
This sequence is the entire insert of clone RP23-129N7.

FEATURES
source
1. .217225
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="15"
/clone="RP23-129N7"
/clone_lib="RPCI-23"
4712. .4781
misc_feature
/note="Sequence from uni-directional dGTP big dye
terminator reads only."
206582. .206603
misc_feature
/note="Sequence from uni-directional primer reads only."

ORIGIN
Alignment Scores:
Pred. No.: 5.63e+03 Length: 217225
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x AL513345 (1-217225)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 122508 GTTCTTGAGGTTGGGTCTTTTGT 122482

RESULT 14
AC119853
LOCUS 236274 bp DNA linear ROD 17-JAN-2004
DEFINITION Mus musculus chromosome 16, clone RP23-231E23, complete sequence.
ACCESSION AC119853
VERSION AC119853.9 GI:41015153
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```



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repeat_region      /rpt_family="MTA"
13531. .14628
/rpt_family="MT-int"
repeat_region      14629. .15023
/rpt_family="MTA"
15783. .16103
/rpt_family="MURVY-int"
repeat_region      16381. .16655
/rpt_family="MURVY-int"
repeat_region      17116. .18775
/rpt_family="MURVY-int"
repeat_region      19088. .19564
/rpt_family="IAPLTR2_MM"
repeat_region      19614. .19825
/rpt_family="MURVY-int"
repeat_region      complement(20880. .21254)
/rpt_family="RMER17C"
repeat_region      22067. .22291
/rpt_family="B4A"
repeat_region      complement(22606. .23019)
/rpt_family="MTC"
repeat_region      23597. .23666
/rpt_family="RMER6A"
repeat_region      23667. .23865
/rpt_family="RMER6A"
repeat_region      23892. .23936
/rpt_family="(TC)n"
repeat_region      23937. .24045
/rpt_family="RMER19B"
repeat_region      complement(24419. .25145)
/rpt_family="ORR1A-int"
repeat_region      complement(25940. .26264)
/rpt_family="MT-int"
repeat_region      complement(26570. .26958)
/rpt_family="L1_MM"
repeat_region      complement(26993. .27042)
/rpt_family="B1_MM"
repeat_region      27055. .27192
/rpt_family="RLTR14"
repeat_region      27345. .27493
/rpt_family="B1_MM"
repeat_region      complement(27799. .27921)
/rpt_family="ID B1"
repeat_region      complement(28034. .28158)
/rpt_family="MLTIC"
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Alignment Scores:

Pred. No.:	6.09e+03	Length:	236274
Score:	45.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	90.00%	Indels:	0
DB:	10	Gaps:	0

US-10-014-101B-40 (1-9) x AC119853 (1-236274)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 51371 GTGTTAGGGGTTTGGGGATTTTTGT 51397

RESULT 15
AC124136/c
LOCUS AC124136 277408 bp DNA linear HTG 23-APR-2003
DEFINITION Mus musculus clone RP23-250H5, WORKING DRAFT SEQUENCE, 8 unordered pieces.
ACCESSION AC124136
VERSION AC124136.3 GI:30017985
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 277408)

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-250H5
Unpublished
2 (bases 1 to 277408)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (09-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 277408)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:28195473.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23602
Center clone name: 250_H_5

TITLE
JOURNAL
COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
* 1 67323: contig of 67323 bp in length
* 67324 67423: gap of 100 bp
* 67424 68625: contig of 1202 bp in length
* 68626 68725: gap of 100 bp
* 68726 77470: contig of 8745 bp in length
* 77471 77570: gap of 100 bp
* 77571 154881: contig of 77311 bp in length
* 154882 154981: gap of 100 bp
* 154982 169669: contig of 14688 bp in length
* 169670 169769: gap of 100 bp
* 169770 197889: contig of 28120 bp in length
* 197890 197989: gap of 100 bp
* 197990 269817: contig of 71828 bp in length
* 269818 269917: gap of 100 bp
* 269918 277408: contig of 7491 bp in length.

FEATURES

source

1. .277408
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-250H5"
/clone_lib="RPCI-23 Female Mouse BAC"
1. .67323
/note="assembly_fragment
clone_end:SP6
vector_side:left"
67424..68625
/note="assembly_fragment"
68726..77470
/note="assembly_fragment"
77571..154881
/note="assembly_fragment"
154882..169669
/note="assembly_fragment"
169770..197889
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197990..269817
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269918..277408
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clone_end:T7
vector_side:right"

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

ORIGIN

Alignment Scores:
Pred. No.: 7.06e+03 Length: 277408
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC124136 (1-277408)

Qy 1 ValLeuGlyLeuGlyGlnPheCys 9

Db 218386 GTGTTAGGGGTTGGGGATTTTTGT. 218360

RESULT 16

E07190/c

LOCUS E07190 1509 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding carotenoid synthetase from Thermus thermophilus.

ACCESSION E07190

VERSION E07190.1 GI:2175331

KEYWORDS JP 1994098774-A/1.

SOURCE Thermus aquaticus

ORGANISM

Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
Thermus.

REFERENCE 1 (bases 1 to 1509)

AUTHORS Hoshino, T. and Nakahara, T.

TITLE GENE DNA FRAGMENT ORIGINATED FROM THERMUS GENUS BACTERIA AND

JOURNAL

COMMENT

PARTICIPATING IN BIOSYNTHESIS OF CAROTENOID AND ITS USE
Patent: JP 1994098774-A 1 12-APR-1994;
MITSUBISHI PETROCHEM CO LTD
OS Thermus thermophilus
PN JP 1994098774-A/1
PD 12-APR-1994
PF 25-SEP-1992 JP 1992256580
PI HOSHINO TAKAYUKI, NAKAHARA TADAATSU
PC C12N15/31,C12N1/20,C12N1/21,C12P23/00,(C12N15/31,C12R1:01), PC
(C12N1/20,
PC C12R1:01), (C12N1/21,C12R1:01), (C12P23/00,C12R1:01); CC
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1. .1509
FT /organism="Thermus thermophilus" FT
FT /strain="HB27",
FT /clone="pCOP1,pCOP2"
FT 5'UTR 1. .59
FT CDS 60. .1103
FT /product="carotenoid biosynthesis from FT
Thermus
thermophilus"
FT 3'UTR 1104. .1509.
FT Location/Qualifiers
1. .1509

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 90.1 Length: 1509
Score: 44.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 88.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x E07190 (1-1509)

Qy 1 ValLeuGlyLeuGlyGlnPheCys 9

Db 61 ATTCTAGCGGCCTCGGGACTTTTGC 35

RESULT 17

AL139349

LOCUS

DEFINITION

AL139349 68743 bp DNA linear PRI 22-FEB-2001
Human DNA sequence from clone RP11-261P9 on chromosome 20 Contains
ESTs, STSs, GSSs and a CpG island. Contains the 3' part of the
STX16 gene for syntaxin 16 and a novel gene for a protein similar
to fly CG7340 and human putative aminopeptidase ZK353.6 in
chromosome 3 (EC 3.4.11.-), complete sequence.

AL139349 GI:11544447

AL139349.36 HTG; aminopeptidase; CG7340; CpG island; syntaxin 16.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 68743)

AUTHORS Moore, M.

Direct Submission

Submitted (20-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Dec 4, 2000 this sequence version replaced gi:11414473.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20> IMPORTANT: This sequence is not the entire insert of clone RP11-261P9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-261P9 is at 68743 in this sequence. The true left end of clone RP4-806M20 is at 51526 in this sequence. The true right end of clone RP5-907D15 is at 100 in this sequence. RP11-261P9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

FEATURES

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
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/clone_lib="RPCI-11.1"
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1699. .2003
/note="AluSq repeat: matches 1. .305 of consensus"
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/note="2 copies 52 mer 96% conserved"
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mRNA

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Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	87.50%	Mismatches:	0
Query Match:	88.00%	Indels:	0
DB:	9	Gaps:	0

US-10-014-101B-40 (1-9) x AC006198 (1-163410)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 123956 ATAGGTGGCTGGGGCAATTCTGT 123979

RESULT 19

AC105162
LOCUS
DEFINITION Mus musculus chromosome 1 clone RP24-92O11 map 1, *** SEQUENCING IN
PROGRESS ***, 4 ordered pieces.
AC105162
AC105162.9 GI:51572058
VERSION HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
TITLE Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
JOURNAL Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
REFERENCE Cooke,P., DeArellano,M., Collins,S., Collymore,A., Cook,A.,
AUTHORS Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
TITLE Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
JOURNAL Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
AUTHORS Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
TITLE Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
JOURNAL MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
REFERENCE McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,

Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 177725)

REFERENCE
AUTHORS
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (27-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 27, 2004 this sequence version replaced gi:50400139.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu

----- Project Information
Center project name: L18779
Center clone name: 92_O_11

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 29639: contig of 29639 bp in length
* 29640 29739: gap of unknown length
* 29740 149715: contig of 119976 bp in length
* 149716 149815: gap of unknown length
* 149816 154590: contig of 4775 bp in length
* 154591 154690: gap of unknown length
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/map="1"
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/clone_lib="RPCI-24 Male Mouse BAC"

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Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC105162 (1-177725)
QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 132244 CTCCTAGGGGGTCTTGGTCAATATGTC 132270

RESULT 20
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DEFINITION Mus musculus chromosome 1, clone RP23-473M13, complete sequence.
ACCESSION AC102630
VERSION AC102630.6 GI:44891043
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 196529)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus chromosome 1, clone RP23-473M13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 196529)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 196529)
REFERENCE
AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,

Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-JAN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 196529)

REFERENCE
AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collimore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
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Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
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Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-MAR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2004 this sequence version replaced gi:40789150.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L19132
Center clone name: 473_M_13

FEATURES

Source

Location/Qualifiers
1. .196529
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/db_xref="taxon:10090"
/chromosome="1"
/map="1"
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/clone_lib="RPCI-23 Female Mouse BAC"
1. .5196
/note="wgs_end_extension
clone_end:SP6"

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repeat_region

repeat_region

repeat_region

repeat_region

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repeat_region

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2754. .2889
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2890. .2957
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3070. .3246
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complement(3247. .3449)
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4738. .4881
/rpt_family="B1F"
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5082. .5102
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5103. .5229
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5197. .5202
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5904. .5965
/rpt_family="(TC)n"
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/rpt_family="B2_Mm2"
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13308. .13488
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14332. .14420
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/rpt_family="B3"
repeat_region
14955. .15073
/rpt_family="PB1D9"
repeat_region
complement(15080. .15235)
/rpt_family="L1MB5"
repeat_region
15896. .15964
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16275. .16370
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16724. .16830
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17269. .17299
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20399. .20684
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20685. .20721
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20773. .20847
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21070. .21425
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repeat_region 22628...22755 /rpt_family="B1F"

Alignment Scores:
Pred. No.: 8.05e+03 Length: 196529
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x AC102630 (1-196529)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
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Db 194599 CTGGAGGATGGGCAGTTTGT 194622

RESULT 21
AE017222/c

LOCUS AE017222 232605 bp DNA circular BCT 10-MAY-2004
DEFINITION Thermus thermophilus HB27 plasmid pTT27, complete sequence.
ACCESSION AE017222
VERSION AE017222.1 GI:46197920
KEYWORDS
SOURCE Thermus thermophilus HB27
ORGANISM Thermus thermophilus HB27
Bacteria; Deinococcus-Thermus; Thermus; Deinococci; Thermales; Thermaceae; Thermus.

REFERENCE 1 (bases 1 to 232605)
AUTHORS Henne,A., Brueggemann,H., Raasch,C., Wierzer,A., Hartsch,T., Liesegang,H., Johann,A., Lienard,T., Gohl,O., Martinez-Arias,R., Jacobi,C., Starkuviene,V., Schlenczek,S., Dencker,S., Huber,R., Klenk,H.-P., Overbeek,R., Kramer,W., Merkl,R., Gottschalk,G. and Fritz,H.-J.
TITLE The genome sequence of the extreme thermophile Thermus thermophilus
JOURNAL Nat. Biotechnol. 22 (5), 547-553 (2004)
PUBMED 15064768

REFERENCE 2 (bases 1 to 232605)
AUTHORS Henne,A., Brueggemann,H., Raasch,C., Wierzer,A., Hartsch,T., Liesegang,H., Johann,A., Lienard,T., Gohl,O., Martinez-Arias,R., Jacobi,C., Starkuviene,V., Schlenczek,S., Dencker,S., Huber,R., Klenk,H.-P., Overbeek,R., Kramer,W., Merkl,R., Gottschalk,G. and Fritz,H.-J.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2004) Goettingen Genomics Laboratory, Institute for Microbiology and Genetics, Grisebachstr. 8, Goettingen D-37077, Germany

FEATURES
source Location/Qualifiers
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/strain="HB27"
/db_xref="taxon:262724"
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complement(301..1623)
/locus_tag="TTP0001"
/codon_start=1
/transl_table=11
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/protein_id="AAS82331.1"
/db_xref="GI:46197921"
/translation="MRLLAAPHSAGKTTVSLALLALRARGLRVQPFKVGPDYIDP
THLEKAAARPYNLDGFDETGLLALFRHGARGADFALIEGVMGLFDGKDRGEVGS
TAQVARLLKAPVALVVDKMGAGSIAPLAGFRDFHPGVRVVGVFANRVGSRHAEIL
KEALKAVGLPLGLWLPQDAPLEPRLHGLVLAGEVAPPLEALRRAFRVDLLEGVRLA
ASAPPLPEARFPLPPRRPRARVAYAWDKAFSYFYEALLEALGAELVPSPLEDE
ALPKAHALLGGYPFLFAELRSANVALREAIRFPGPVIAECGGMYLSQGLWVGER
FFPVGVLVPGEARMAERPVLGYREVEALRDSVPARKQAQFKGHEFYARLPASPSPAW
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complement(1623..2186)
/locus_tag="TTP0002"

gene

CDS
complement(1623..2186)
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/db_xref="GI:46197922"
/translation="MEEPKRQKPYAKPQGERRGLLVYTDGKGKSTAAFGALRAHG
RGLKVRIFQFIKHGTARFGEHRAFSLLGIPIEGLDGFTWRSRDLARSAALAQEGWGR
AKEALLSGTYDLVLDDEATYPLRYGWSLEEFLEVLRARPPHVHVVTGRTGAPEALDE
LADTVTEMRKVKHAFDQGVPAQRGIEH"
complement(2218..2754)
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ELREREARLEERFHGLEKRIQEVETKLESRIQNLRLGRQIQETETRLGTRIQVEA
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LYLTAVGVVLALLSVFFR"
complement(2759..3478)
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/codon_start=1
/transl_table=11
/product="cobalamin [5'-phosphate] synthase"
/protein_id="AAS82334.1"
/db_xref="GI:46197924"
/translation="MKAFLRALALLTVLPLAPKGVGEEDFKRSVAFFFLAGYLLGLPL
ALLALLPLPPGLSAAAGVALLGLTGFLHLDGLDLADALLGARPREERLRILKDPHL
GAFAGVGGVYLLLFQALALVQDPLFLLLPFGWARFAFLPFLHRYPLLPGMGMAALVR
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LGRGAVVAAADHGVAEGVSAYPQEVTRQMVNLNPLSGGAAINQFALTADCAVYVLDV
GVVGELPDHPGLKRVKRPGTANLARGPAMTPBEAERALLAGREARRAIAGEATILLA
AGDMGIGNTTAAALTAALLGLPPEAVVGRGTGVGEEGLRRKREAVARALARLHPGMG
PLEVAAEVGGLELVAIAGVYLEGYAGLPLVLDGFPVVTAGALLAWKMAPGLRDHLFAG
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4509..5042
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/db_xref="GI:46197926"
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LPAFSSDLLRARTAEIAGFSRLYPELREIHFGALEGALWETLDPRYKEALLRFQGF
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5307..5969
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5307..5969

gene

/locus_tag="TTP0007"
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/transl_table=11
/product="hypothetical conserved protein"
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/db_xref="GI:46197927"
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PLLLGVFLGFGFETASQLSALASAELSPLRLGFAFTLGLMLLVGDVGLLASRLQNL
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PA"

gene

5966. .7066
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/protein_id="AAS82338.1"
/db_xref="GI:46197928"

CDS

/translation="MSHPYPPPRDKKSGRIGFTTGANAAAAAALALLGEAPVVVD
IWLPAWRQPFRVRLERKGDGLVGMIKDAGDDPDVTHGAEIQAFVRFASEDRLEGG
EUGVWTKPGLGVGEPAINPVRMMIWEAVRETPRLAVTIAIPGGEELAKKTLN
PRLGILGLSVLGTGVVKPYSTSAFRMSVVQAVGARANGILLEIAATTGKSERFAQ
RLPLHPEMAFIEMGDFVDVLRRAARKVGEVVRVGMIGKISKMDGKTMTHAAGGE
VNLISLLSLLKEAGASPKALKAEAGATARRFLEIALEEGLELFFVNLVRLAQEKLQA
YIGERPFVSVALTDFDEGRCLAAPDREYRG"

gene

7059. .7757
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/codon_start=1
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/product="precorrin-8X methylmutase"
/protein_id="AAS82339.1"
/db_xref="GI:46197929"

CDS

/translation="MDDLKAQKNPAHQMTKEGRAIEEESFRIVDOEAGPHGFSPLEW
PVVRMIHATADFEYKALTRFSQGAVEAGLKAIQAGARILVDARMIACGLNPERLRLF
INEVVELLAHPEVVVARAKATGGTRAEAAVAYAEKGLLDGAIVGVGNAPTFLALVEA
IRQGARPALVLGMPGVFNVLAKRALMEAPVPWIVTEGRKGGSTLVVAALHALIRLA
ADGGVDTSRAYREG"

gene

7758. .8969
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7758. .8969
/locus_tag="TTP0010"
/EC_number="2.1.1.132"
/codon_start=1
/transl_table=11
/product="precorrin-6Y C5,15-methyltransferase
[decarboxylating]"

CDS

/protein_id="AAS82340.1"
/db_xref="GI:46197930"
/translation="MVYVIGMGARGREGLSKALRRLEEAENVLIGRRHLAHFPDHPG
EKVPVQGPLEALLDLAEARKKEGKVAFLASGDPLFYGIGKRVLERFPEAEVHPAPTA
FQEAFARLKLPWDQARFFSLHGRPLGGVLLLELSPLSVVYTDPEHTPAGIARALLEM
GVDARAHVAERLGEEDERVRSFAGLKEVAEERFLDPNVLILEAKGFLPRLGFFPDEA
FEQRMPPKKGLITKREVRLLALGLLPPDGVLDIGAGTSGVGEIARLAPWGEVYAV
EKNPESWPHIVENARRFGAFNLHLVKGEAPEALKGLPAPHAVFVGSGGELEELRVS
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ITLLAVTKEGA"

gene

8966. .9637
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/transl_table=11
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/protein_id="AAS82341.1"
/db_xref="GI:46197931"

CDS

Alignment Scores:
Pred. No.: 9.4e+03 Length: 232605
Score: 44.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 88.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-40 (1-9) x AE017222 (1-232605)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 51636 ATTCTAGCGGCCTCGGGGACTTTTGC 51610

RESULT 22

AY661656/c

LOCUS AY661656 279448 bp DNA linear PLN 03-JUL-2004
DEFINITION Sorghum bicolor clone BAC 88M4, complete sequence.

ACCESSION AY661656

VERSION AY661656.1 GI:49359135

KEYWORDS HTG.

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 279448)

AUTHORS Islam-Faridi,M.N., Kim,J.-S., Klein,P.E., Stelly,D.M., Price,H.J.,
Klein,R.R. and Mullet,J.E.

TITLE Cytogenetic Analysis of Sorghum Chromosome 3 and Alignment to Rice

Chromosome 1 Reveals Expansion of Pericentromeric Heterochromatin
in Sorghum

JOURNAL Unpublished (2004)

REFERENCE 2 (bases 1 to 279448)

AUTHORS Klein,R.R., Klein,P.E., Mullet,J.E., Minx,P. and Miner,T.L.

TITLE Direct Submission

JOURNAL Submitted (21-JUN-2004) USDA-ARS, Southern Plains Agricultural
Research Center, 2765 F&B Road, College Station, TX 77845, USA

FEATURES

source

1. .279448
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="IS3620C"
/db_xref="taxon:4558"
/chromosome="8"
/map="104.2-111.2 cM"
/clone="BAC 88M4"

ORIGIN

Alignment Scores:

Pred. No.: 1.11e+04 Length: 279448
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-40 (1-9) x AY661656 (1-279448)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 51903 TTGGAGGCATGGGGCAGTTTGT 51880

RESULT 23

AR042369/c

LOCUS AR042369 5183 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 3 from patent US 5811304.

ACCESSION AR042369

VERSION AR042369.1 GI:5962865

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 5183)
AUTHORS Huang,S.
TITLE Nucleic acid molecules encoding retinoblastoma protein-interacting zinc finger proteins
JOURNAL Patent: US 5811304-A 3 22-SEP-1998;
FEATURES Location/Qualifiers
source 1..5183
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 441 Length: 5183
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x AR042369 (1-5183)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 1608 GTTCTGGGTGGCCTGGCCTGTTCTGC 1582

RESULT 24
AR052277/c
LOCUS AR052277 5183 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5831008.
ACCESSION AR052277
VERSION AR052277.1 GI:5975641
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5183)
AUTHORS Huang,S.
TITLE Retinoblastoma protein-interacting zinc finger proteins
JOURNAL Patent: US 5831008-A 3 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..5183
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 441 Length: 5183
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x AR052277 (1-5183)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 1608 GTTCTGGGTGGCCTGGCCTGTTCTGC 1582

RESULT 25
AR241188/c
LOCUS AR241188 5868 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6468985.
ACCESSION AR241188
VERSION AR241188.1 GI:27286418
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5868)
AUTHORS Huang,S.
TITLE Retinoblastoma protein-interacting zinc finger proteins

JOURNAL Patent: US 6468985-A 3 22-OCT-2002;
FEATURES Location/Qualifiers
source 1..5868
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 494 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x AR241188 (1-5868)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 1728 GTTCTGGGTGGCCTGGCCTGTTCTGC 1702

RESULT 26
AR262645/c
LOCUS AR262645 5868 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 6323335.
ACCESSION AR262645
VERSION AR262645.1 GI:28074187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5868)
AUTHORS Huang,S.
TITLE Retinoblastoma protein-interacting zinc finger proteins
JOURNAL Patent: US 6323335-A 3 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..5868
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 494 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x AR262645 (1-5868)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 1728 GTTCTGGGTGGCCTGGCCTGTTCTGC 1702

RESULT 27
AX346724
LOCUS AX346724 6113 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 1795 from Patent WO0200928.
ACCESSION AX346724
VERSION AX346724.1 GI:18494610
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 1795 03-JAN-2002;
FEATURES Location/Qualifiers
source 1..6113
/organism="synthetic construct"

ORIGIN

that may function as a transcription factor for the human heme-oxygenase-1 gene
Eur. J. Biochem. 235 (3), 471-479 (1996)
96184519
8654390
2 (bases 1 to 6188)
Shibahara, S.
Direct Submission
Submitted (11-JAN-1995) Shigeki Shibahara, Tohoku University School of Medicine, Dept. of Applied Physiol. and Mol. Biol.; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980, Japan (Tel:022-717-8117, Fax:022-717-8118)
On Jul 6, 1996 this sequence version replaced gi:1389628.
Sequence updated (30-May-96) by : Shigeki Shibahara.

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

CDS

US-10-014-101B-40 (1-9) x AX346724 (1-6113)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 5780 GTTTGGTGGGTAGGTGTTTGT 5806

RESULT 28
CQ715456/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE

JOURNAL

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 513 Length: 6113
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x AX346724 (1-6113)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 5780 GTTTGGTGGGTAGGTGTTTGT 5806

RESULT 28
CQ715456/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE

JOURNAL

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 518 Length: 6177
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x CQ715456 (1-6177)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 1182 GTTCTGGTGGCCTGGGCCTGTTCTGC 1156

RESULT 29
HUMHOXY1/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE

that may function as a transcription factor for the human heme-oxygenase-1 gene
Eur. J. Biochem. 235 (3), 471-479 (1996)
96184519
8654390
2 (bases 1 to 6188)
Shibahara, S.
Direct Submission
Submitted (11-JAN-1995) Shigeki Shibahara, Tohoku University School of Medicine, Dept. of Applied Physiol. and Mol. Biol.; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980, Japan (Tel:022-717-8117, Fax:022-717-8118)
On Jul 6, 1996 this sequence version replaced gi:1389628.
Sequence updated (30-May-96) by : Shigeki Shibahara.

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

CDS

US-10-014-101B-40 (1-9) x HUMHOXY1 (1-6188)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 1182 GTTCTGGTGGCCTGGGCCTGTTCTGC 1156

RESULT 30
AX345583
LOCUS
DEFINITION
ACCESSION

ORIGIN

Alignment Scores:
Pred. No.: 519 Length: 6188
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-40 (1-9) x HUMHOXY1 (1-6188)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 1182 GTTCTGGTGGCCTGGGCCTGTTCTGC 1156

RESULT 30
AX345583
LOCUS
DEFINITION
ACCESSION

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VERSION      AX345583.1  GI:18493469
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Olek,A., Piepenbrock,C. and Berlin,K.
TITLE        Diagnosis of diseases associated with the immune system
JOURNAL      Patent: WO 0200928-A 654 03-JAN-2002;
              Epigenomics AG (DE)
FEATURES     Location/Qualifiers
              source
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                /note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN
Alignment Scores:
Pred. No.:      538      Length:      6436
Score:          43.00    Matches:      8
Percent Similarity: 88.89%  Conservative: 0
Best Local Similarity: 88.89%  Mismatches: 1
Query Match:    86.00%      Indels:      0
DB:             6          Gaps:      0

US-10-014-101B-40 (1-9) x AX345583 (1-6436)

QY      1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db      5764 GTTTGGGTGGGTAGGTGTTTTCG 5790

RESULT 31
AX780015/c
LOCUS      AX780015      6704 bp      DNA      linear      PAT 14-JUL-2003
DEFINITION Sequence 2172 from Patent WO03039443.
ACCESSION  AX780015
VERSION     AX780015.1  GI:32697009
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
              Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
TITLE        Novel genetic markers for leukemias
JOURNAL      Patent: WO 03039443-A 2172 15-MAY-2003;
              Deutsches Krebsforschungszentrum (DE) ;
              Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
              PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES     Location/Qualifiers
              source
                1..6704
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:      559      Length:      6704
Score:          43.00    Matches:      8
Percent Similarity: 88.89%  Conservative: 0
Best Local Similarity: 88.89%  Mismatches: 1
Query Match:    86.00%      Indels:      0
DB:             6          Gaps:      0

US-10-014-101B-40 (1-9) x AX780015 (1-6704)

QY      1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db      1476 GTTCTGGGTGGCTGGGCTGTTCTGC 1450

RESULT 32
VERSION      AX281287
KEYWORDS     .
SOURCE       Sequence 29 from Patent WO0177164.
ORGANISM     AX281287
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Olek,A., Piepenbrock,C. and Berlin,K.
TITLE        Diagnosis of diseases associated with apoptosis
JOURNAL      Patent: WO 0177164-A 29 18-OCT-2001;
              Epigenomics AG (DE)
FEATURES     Location/Qualifiers
              source
                1..7603
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ORIGIN
Alignment Scores:
Pred. No.:      628      Length:      7603
Score:          43.00    Matches:      8
Percent Similarity: 88.89%  Conservative: 0
Best Local Similarity: 88.89%  Mismatches: 1
Query Match:    86.00%      Indels:      0
DB:             6          Gaps:      0

US-10-014-101B-40 (1-9) x AX281287 (1-7603)

QY      1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db      334 GTTTGGGTGGGTAGGTGTTTGT 360

RESULT 33
AX345210
LOCUS      AX345210      7603 bp      DNA      linear      PAT 01-FEB-2002
DEFINITION Sequence 281 from Patent WO0200928.
ACCESSION  AX345210
VERSION     AX345210.1  GI:18493096
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Olek,A., Piepenbrock,C. and Berlin,K.
TITLE        Diagnosis of diseases associated with the immune system
JOURNAL      Patent: WO 0200928-A 281 03-JAN-2002;
              Epigenomics AG (DE)
FEATURES     Location/Qualifiers
              source
                1..7603
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN
Alignment Scores:
Pred. No.:      628      Length:      7603
Score:          43.00    Matches:      8
Percent Similarity: 88.89%  Conservative: 0
Best Local Similarity: 88.89%  Mismatches: 1
Query Match:    86.00%      Indels:      0
DB:             6          Gaps:      0

US-10-014-101B-40 (1-9) x AX345210 (1-7603)

QY      1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db      334 GTTTGGGTGGGTAGGTGTTTGT 360
```


RESULT 34
HSU17838/c
LOCUS
DEFINITION Homo sapiens zinc finger protein RIZ mRNA, complete cds.
ACCESSION U17838
VERSION U17838.1 GI:1669774
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Buyse,I.M., Shao,G. and Huang,S.
TITLE The retinoblastoma protein binds to RIZ, a zinc-finger protein that shares an epitope with the adenovirus E1A protein
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (10), 4467-4471 (1995)
MEDLINE 95273384
PUBMED 7538672
REFERENCE
AUTHORS Huang,S.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1994) Shi Huang, La Jolla Cancer Research Foundation, 10901 N. Torrey Pines Road, La Jolla, CA 92037, USA
REFERENCE
AUTHORS Huang,S.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2000) Shi Huang, La Jolla Cancer Research Foundation, 10901 N. Torrey Pines Road, La Jolla, CA 92037, USA
REMARK Amino acid sequence updated by submitter
COMMENT On Nov 15, 1996 this sequence version replaced gi:949997.
FEATURES
source
1. .7942
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/protein_id="AAC50820.2"
/db_xref="GI:9955379"
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LGPDCILMNSEKASQDTINSSVVEENGVEKELHPCKYCKKVFGTHTNMRRHQRVHER
HLIPKGVRRKGLEEQPAEQAQATQNVVYPSPEEEGEADDVYIMDISNISENL
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SPCKSLEAQPDPDLGPGSGFPAPTESTPDVCPSSPALQTPSLSSGQLPPLLIPTDPS
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Alignment Scores:
Pred. No.: 654 Length: 7942
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-40 (1-9) x HSU17838 (1-7942)
Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
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Db 2463 GTTCTGGTGGCCTGGGCCTGTTCTGC 2437
RESULT 35
AX323793
LOCUS AX323793 9504 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 281 from Patent WO0192565.
ACCESSION AX323793
VERSION AX323793.1 GI:18094541
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with dna transcription
JOURNAL Patent: WO 0192565-A 281 06-DEC-2001;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
1. .9504
/organism="synthetic construct"
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Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-40 (1-9) x AX323793 (1-9504)
Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 6626 GTTTGGTGGGTTAGGTGTTTTTGT 6652
RESULT 36
AC023042/c
LOCUS AC023042 55622 bp DNA linear HTG 30-JUL-2002
DEFINITION Homo sapiens clone RP11-141M19, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC023042
VERSION AC023042.3 GI:22004286
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 55622)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-141M19
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 55622)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepl,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,

Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

Direct Submission

Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 55622)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,N., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 30, 2002 this sequence version replaced gi:7263244.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L941

Center clone name: 141_M_19

* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 665: contig of 665 bp in length
* 666
* 765: gap of 100 bp
* 766 1446: contig of 681 bp in length
* 1447 1546: gap of 100 bp
* 1547 2243: contig of 697 bp in length
* 2244 2343: gap of 100 bp
* 2344 3036: contig of 693 bp in length
* 3037 3136: gap of 100 bp
* 3137 3805: contig of 669 bp in length
* 3806 3905: gap of 100 bp
* 3906 4586: contig of 681 bp in length
* 4587 4686: gap of 100 bp
* 4687 5348: contig of 662 bp in length

5349 5448: gap of 100 bp
* 5449 6141: contig of 693 bp in length
* 6142 6241: gap of 100 bp
* 6242 6931: contig of 690 bp in length
* 6932 7031: gap of 100 bp
* 7032 7723: contig of 692 bp in length
* 7724 7823: gap of 100 bp
* 7824 8519: contig of 696 bp in length
* 8520 8619: gap of 100 bp
* 8620 9315: contig of 696 bp in length
* 9316 9415: gap of 100 bp
* 9416 10116: contig of 701 bp in length
* 10117 10216: gap of 100 bp
* 10217 10890: contig of 674 bp in length
* 10891 10990: gap of 100 bp
* 10991 11656: contig of 676 bp in length
* 11667 11766: gap of 100 bp
* 11767 12437: contig of 671 bp in length
* 12438 12537: gap of 100 bp
* 12538 13230: contig of 693 bp in length
* 13231 13330: gap of 100 bp
* 13331 14016: contig of 686 bp in length
* 14017 14116: gap of 100 bp
* 14117 14802: contig of 686 bp in length
* 14803 14902: gap of 100 bp
* 14903 15565: contig of 663 bp in length
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* 17912 18011: gap of 100 bp
* 18012 18697: contig of 686 bp in length
* 18698 18797: gap of 100 bp
* 18798 19491: contig of 694 bp in length
* 19492 19591: gap of 100 bp
* 19592 20264: contig of 673 bp in length
* 20265 20364: gap of 100 bp
* 20365 21055: contig of 691 bp in length
* 21056 21155: gap of 100 bp
* 21156 21850: contig of 695 bp in length
* 21851 22634: contig of 684 bp in length
* 22635 22734: gap of 100 bp
* 22735 23389: contig of 655 bp in length
* 23390 23489: gap of 100 bp
* 23490 24172: contig of 683 bp in length
* 24173 24272: gap of 100 bp
* 24273 24962: contig of 690 bp in length
* 24963 25062: gap of 100 bp
* 25063 25751: contig of 689 bp in length
* 25752 25851: gap of 100 bp
* 25852 26523: contig of 672 bp in length
* 26524 26623: gap of 100 bp
* 26624 27320: contig of 697 bp in length
* 27321 27420: gap of 100 bp
* 27421 28086: contig of 666 bp in length
* 28087 28186: gap of 100 bp
* 28187 28868: contig of 682 bp in length
* 28869 28968: gap of 100 bp
* 28969 29649: contig of 681 bp in length
* 29650 29749: gap of 100 bp
* 29750 30440: contig of 691 bp in length
* 30441 30540: gap of 100 bp
* 30541 31230: contig of 690 bp in length
* 31231 31330: gap of 100 bp
* 31331 32013: contig of 683 bp in length
* 32014 32113: gap of 100 bp
* 32114 32800: contig of 687 bp in length
* 32801 32900: gap of 100 bp
* 32901 33590: contig of 690 bp in length
* 33591 33690: gap of 100 bp

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* 34486	35178:	contig of 693	bp in length
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* 35279	35964:	contig of 686	bp in length
* 35965	36064:	gap of 100	bp
* 36065	36763:	contig of 699	bp in length
* 36764	36863:	gap of 100	bp
* 36864	37522:	contig of 659	bp in length
* 37523	37622:	gap of 100	bp
* 37623	38295:	contig of 673	bp in length
* 38296	38395:	gap of 100	bp
* 38396	39028:	contig of 633	bp in length
* 39029	39128:	gap of 100	bp
* 39129	39810:	contig of 682	bp in length
* 39811	39910:	gap of 100	bp
* 39911	40581:	contig of 671	bp in length
* 40582	40681:	gap of 100	bp
* 40682	41363:	contig of 682	bp in length
* 41364	41463:	gap of 100	bp
* 41464	42150:	contig of 687	bp in length
* 42151	42250:	gap of 100	bp
* 42251	42921:	contig of 671	bp in length
* 42922	43021:	gap of 100	bp
* 43022	43705:	contig of 684	bp in length
* 43706	43805:	gap of 100	bp
* 43806	44493:	contig of 688	bp in length
* 44494	44593:	gap of 100	bp
* 44594	45285:	contig of 692	bp in length
* 45286	45385:	gap of 100	bp
* 45386	46072:	contig of 687	bp in length
* 46073	46172:	gap of 100	bp
* 46173	46864:	contig of 692	bp in length
* 46865	46964:	gap of 100	bp

Alignment Scores:

Pred. No.:	3.94e+03	Length:	55622
Score:	43.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	87.50%	Mismatches:	0
Query Match:	86.00%	Indels:	0
DB:	2	Gaps:	0

US-10-014-101B-40 (1-9) x AC023042 (1-55622)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 43326 CTGGGAGGCTCTGGAGAAATTTTGC 43303

RESULT 37

AC091556

LOCUS

DEFINITION Homo sapiens chromosome 12 clone RP11-401110 map 12, LOW-PASS HTG 28-AUG-2002

SEQUENCE SAMPLING.

ACCESSION AC091556

VERSION AC091556.1 GI:13959161

KEYWORDS HTG; HTGS_PHASE0.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 59433)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 12, clone RP11-401110

Unpublished

2 (bases 1 to 59433)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,

Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,

Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,

Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,

Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

3 (bases 1 to 59433)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
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Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L11612

Center clone name: 401_I_10

* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 740: contig of 740 bp in length

* 741 840: gap of 100 bp

* 841 1601: contig of 761 bp in length

* 1602 1701: gap of 100 bp

* 1702 2413: contig of 712 bp in length

* 2414 2513: gap of 100 bp

* 2514 3246: contig of 733 bp in length

* 3247 3346: gap of 100 bp

* 3347 4060: contig of 714 bp in length
* 4061 4160: gap of 100 bp
* 4161 4911: contig of 751 bp in length
* 4912 5011: gap of 100 bp
* 5012 5767: contig of 756 bp in length
* 5768 5867: gap of 100 bp
* 5868 6623: contig of 756 bp in length
* 6624 6723: gap of 100 bp
* 6724 7481: contig of 758 bp in length
* 7482 7581: gap of 100 bp
* 7582 8324: contig of 743 bp in length
* 8325 8424: gap of 100 bp
* 8425 9122: contig of 698 bp in length
* 9123 9222: gap of 100 bp
* 9223 9965: contig of 743 bp in length
* 9966 10065: gap of 100 bp
* 10066 10773: contig of 708 bp in length
* 10774 10873: gap of 100 bp
* 10874 11595: contig of 722 bp in length
* 11596 11695: gap of 100 bp
* 11696 12433: contig of 738 bp in length
* 12434 12533: gap of 100 bp
* 12534 13270: contig of 737 bp in length
* 13271 13370: gap of 100 bp
* 13371 14120: contig of 750 bp in length
* 14121 14220: gap of 100 bp
* 14221 14946: contig of 726 bp in length
* 14947 15046: gap of 100 bp
* 15047 15811: contig of 765 bp in length
* 15812 15911: gap of 100 bp
* 15912 16640: contig of 729 bp in length
* 16641 16740: gap of 100 bp
* 16741 17439: contig of 699 bp in length
* 17440 17539: gap of 100 bp
* 17540 18271: contig of 732 bp in length
* 18272 18371: gap of 100 bp
* 18372 19133: contig of 762 bp in length
* 19134 19233: gap of 100 bp
* 19234 19986: contig of 753 bp in length
* 19987 20086: gap of 100 bp
* 20087 20849: contig of 763 bp in length
* 20850 20949: gap of 100 bp
* 20950 21709: contig of 760 bp in length
* 21710 21809: gap of 100 bp
* 21810 22563: contig of 754 bp in length
* 22564 22663: gap of 100 bp
* 22664 23381: contig of 718 bp in length
* 23382 23481: gap of 100 bp
* 23482 24229: contig of 748 bp in length
* 24230 24329: gap of 100 bp
* 24330 25067: contig of 738 bp in length
* 25068 25167: gap of 100 bp
* 25168 25896: contig of 729 bp in length
* 25897 25996: gap of 100 bp
* 25997 26754: contig of 758 bp in length
* 26755 26854: gap of 100 bp
* 26855 27586: contig of 732 bp in length
* 27587 27686: gap of 100 bp
* 27687 28427: contig of 741 bp in length
* 28428 28527: gap of 100 bp
* 28528 29292: contig of 765 bp in length
* 29293 29392: gap of 100 bp
* 29393 30153: contig of 761 bp in length
* 30154 30253: gap of 100 bp
* 30254 31004: contig of 751 bp in length
* 31005 31104: gap of 100 bp
* 31105 31858: contig of 754 bp in length
* 31859 31958: gap of 100 bp
* 31959 32700: contig of 742 bp in length
* 32701 32800: gap of 100 bp
* 32801 33526: contig of 726 bp in length
* 33527 33626: gap of 100 bp
* 33627 34396: contig of 770 bp in length

* 34397 34496: gap of 100 bp
* 34497 35244: contig of 748 bp in length
* 35245 35344: gap of 100 bp
* 35345 36086: contig of 742 bp in length
* 36087 36186: gap of 100 bp
* 36187 36956: contig of 770 bp in length
* 36957 37056: gap of 100 bp
* 37057 37817: contig of 761 bp in length
* 37818 37917: gap of 100 bp
* 37918 38658: contig of 741 bp in length
* 38659 38758: gap of 100 bp
* 38759 39505: contig of 747 bp in length
* 39506 39605: gap of 100 bp
* 39606 40342: contig of 737 bp in length
* 40343 40442: gap of 100 bp
* 40443 41154: contig of 712 bp in length
* 41155 41254: gap of 100 bp
* 41255 41839: contig of 585 bp in length
* 41840 41939: gap of 100 bp
* 41940 42679: contig of 740 bp in length
* 42680 42779: gap of 100 bp
* 42780 43510: contig of 731 bp in length
* 43511 43610: gap of 100 bp
* 43611 44361: contig of 751 bp in length
* 44362 44461: gap of 100 bp
* 44462 45222: contig of 761 bp in length
* 45223 45322: gap of 100 bp
* 45323 46061: contig of 739 bp in length
* 46062 46161: gap of 100 bp
* 46162 46901: contig of 740 bp in length
* 46902 47001: gap of 100 bp
* 47002 47764: contig of 763 bp in length

Alignment Scores:

Pred. No.: 4.19e+03 Length: 59433
Score: 43.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 86.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC091556 (1-59433)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 18622 CTGGAGGCTCTTGGAGAAATTTGC 18645

RESULT 38

AC011925

LOCUS

DEFINITION

AC011925

AC011925

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 76891)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouckhelter,B.,

Brown,A., Castelle,A., Colangelo,M., Collins,S., Collymore,A.,

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Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Holwand,J.C., Johnson,R., Jones,C., Kann,B., Karatas,A., Klein,J.,

Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

AC011925 76891 bp DNA linear HTG 13-JUL-2000
Homo sapiens clone RP11-15M20, LOW-PASS SEQUENCE SAMPLING.

AC011925.2 GI:7144915

HTG; HTGS_PHASE0.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 76891)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouckhelter,B.,

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Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Holwand,J.C., Johnson,R., Jones,C., Kann,B., Karatas,A., Klein,J.,

Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (16-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6056258.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3490

Center clone name: 15_M_20

* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 876: contig of 876 bp in length
877 976: gap of 100 bp
977 1877: contig of 901 bp in length
1878 1977: gap of 100 bp
1978 2831: contig of 854 bp in length
2832 2931: gap of 100 bp
2932 3752: contig of 821 bp in length
3753 3852: gap of 100 bp
3853 4693: contig of 841 bp in length
4694 4793: gap of 100 bp
4794 5632: contig of 839 bp in length
5633 5732: gap of 100 bp
5733 6586: contig of 854 bp in length
6587 6686: gap of 100 bp
6687 7526: contig of 840 bp in length
7527 7626: gap of 100 bp
7627 8483: contig of 857 bp in length
8484 8583: gap of 100 bp
8584 9424: contig of 841 bp in length
9425 9524: gap of 100 bp
9525 10382: contig of 858 bp in length
10383 10482: gap of 100 bp
10483 11355: contig of 873 bp in length
11356 11455: gap of 100 bp
11456 12330: contig of 875 bp in length
12331 12430: gap of 100 bp
12431 13230: contig of 800 bp in length
13231 13330: gap of 100 bp
13331 14172: contig of 842 bp in length
14173 14272: gap of 100 bp
14273 15104: contig of 832 bp in length
15105 15204: gap of 100 bp
15205 16034: contig of 830 bp in length
16035 16134: gap of 100 bp
16135 16945: contig of 811 bp in length
16946 17045: gap of 100 bp
17046 17860: contig of 815 bp in length
17861 17960: gap of 100 bp
17961 18842: contig of 882 bp in length
18843 18942: gap of 100 bp
18943 19801: contig of 859 bp in length
19802 19901: gap of 100 bp

19902 20749: contig of 848 bp in length
20750 20849: gap of 100 bp
20850 21703: contig of 854 bp in length
21704 21803: gap of 100 bp
21804 22671: contig of 868 bp in length
22672 22771: gap of 100 bp
22772 23613: contig of 842 bp in length
23614 23713: gap of 100 bp
23714 24574: contig of 861 bp in length
24575 24674: gap of 100 bp
24675 25527: contig of 853 bp in length
25528 25627: gap of 100 bp
25628 26478: contig of 851 bp in length
26479 26578: gap of 100 bp
26579 27429: contig of 851 bp in length
27430 27529: gap of 100 bp
27530 28382: contig of 853 bp in length
28383 28482: gap of 100 bp
28483 29360: contig of 878 bp in length
29361 29460: gap of 100 bp
29461 30284: contig of 824 bp in length
30285 30384: gap of 100 bp
30385 31252: contig of 868 bp in length
31253 31352: gap of 100 bp
31353 32218: contig of 866 bp in length
32219 32318: gap of 100 bp
32319 33150: contig of 832 bp in length
33151 33250: gap of 100 bp
33251 34083: contig of 833 bp in length
34084 34183: gap of 100 bp
34184 34971: contig of 788 bp in length
34972 35071: gap of 100 bp
35072 35896: contig of 825 bp in length
35897 35996: gap of 100 bp
35997 36872: contig of 876 bp in length
36873 36972: gap of 100 bp
36973 37855: contig of 883 bp in length
37856 37955: gap of 100 bp
37956 38789: contig of 834 bp in length
38790 38889: gap of 100 bp
38890 39747: contig of 858 bp in length
39748 39847: gap of 100 bp
39848 40719: contig of 872 bp in length
40720 40819: gap of 100 bp
40820 41690: contig of 871 bp in length
41691 41790: gap of 100 bp
41791 42639: contig of 849 bp in length
42640 42739: gap of 100 bp
42740 43581: contig of 842 bp in length
43582 43681: gap of 100 bp
43682 44476: contig of 795 bp in length
44477 44576: gap of 100 bp
44577 45396: contig of 820 bp in length
45397 45496: gap of 100 bp
45497 46329: contig of 833 bp in length
46330 46429: gap of 100 bp
46430 47294: contig of 865 bp in length
47295 47394: gap of 100 bp
47395 48258: contig of 864 bp in length
48259 48358: gap of 100 bp
48359 49197: contig of 839 bp in length
49198 49297: gap of 100 bp
49298 50178: contig of 881 bp in length
50179 50278: gap of 100 bp
50279 51141: contig of 863 bp in length
51142 51241: gap of 100 bp
51242 52114: contig of 873 bp in length
52115 52214: gap of 100 bp
52215 53049: contig of 835 bp in length
53050 53149: gap of 100 bp
53150 53998: contig of 849 bp in length
53999 54098: gap of 100 bp
54099 54934: contig of 836 bp in length

* 54935 55034: gap of 100 bp
* 55035 55877: contig of 843 bp in length
* 55878 55977: gap of 100 bp
* 55978 56845: contig of 868 bp in length
* 56846 56945: gap of 100 bp
* 56946 57814: contig of 869 bp in length
* 57815 57914: gap of 100 bp
* 57915 58758: contig of 844 bp in length
* 58759 58858: gap of 100 bp
* 58859 59721: contig of 863 bp in length
* 59722 59821: gap of 100 bp
* 59822 60707: contig of 886 bp in length
* 60708 60807: gap of 100 bp
* 60808 61626: contig of 819 bp in length
* 61627 61726: gap of 100 bp
* 61727 62587: contig of 861 bp in length
* 62588 62687: gap of 100 bp
* 62688 63531: contig of 844 bp in length
* 63532 63631: gap of 100 bp
* 63632 64470: contig of 839 bp in length
* 64471 64570: gap of 100 bp
* 64571 65403: contig of 833 bp in length
* 65404 65503: gap of 100 bp
* 65504 66374: contig of 871 bp in length
* 66375 66474: gap of 100 bp
* 66475 67375: contig of 901 bp in length
* 67376 67475: gap of 100 bp
* 67476 68349: contig of 874 bp in length
* 68350 68449: gap of 100 bp
* 68450 69305: contig of 856 bp in length

Alignment Scores:
Pred. No.: 5.31e+03 Length: 76891
Score: 43.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 86.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC011925 (1-76891)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 13808 TTGGGTGCTCTGGGCAATCTGC 13831

RESULT 39
AC020850_3
WPCOMMENT

Sequence split into 5 fragments LOCUS AC020850 Accession AC020850
Fragment Name Begin End
AC020850_0 1 110000
AC020850_1 100001 210000
AC020850_2 200001 310000
AC020850_3 300001 410000
AC020850_4 400001 444882
Continuation (4 of 5) of AC020850 from base 300001 (AC020850 Mus musculus clone RP21-460)

Alignment Scores:
Pred. No.: 7.39e+03 Length: 110000
Score: 43.00 Matches: 7
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 0
Query Match: 86.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC020850_3 (1-110000)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 87394 CTTCTGGGAGGCTTAGGCAGGTTTGT 87420

RESULT 40
AC024999

LOCUS AC024999 132446 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens chromosome 1 clone RP11-178K15 map 1, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC024999
VERSION AC024999.2 GI:7767841
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 132446)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 1, clone RP11-178K15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 132446)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

DIRECT SUBMISSION

TITLE

JOURNAL

COMMENT

Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 10, 2000 this sequence version replaced gi:7145043.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7587

Center clone name: 178_K_15

* NOTE: This record contains 146 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 757: contig of 757 bp in length
* 758 857: gap of 100 bp
* 858 1609: contig of 752 bp in length
* 1610 1709: gap of 100 bp
* 1710 2474: contig of 765 bp in length
* 2475 2574: gap of 100 bp
* 2575 3319: contig of 745 bp in length
* 3320 3419: gap of 100 bp
* 3420 4160: contig of 741 bp in length
* 4161 4260: gap of 100 bp

* 4261 5007: contig of 747 bp in length
* 5008 5107: gap of 100 bp
* 5108 5850: contig of 743 bp in length
* 5851 5950: gap of 100 bp
* 5951 6690: contig of 740 bp in length
* 6691 6790: gap of 100 bp
* 6791 7540: contig of 750 bp in length
* 7541 7640: gap of 100 bp
* 7641 8365: contig of 725 bp in length
* 8366 8465: gap of 100 bp
* 8466 9236: contig of 771 bp in length
* 9237 9336: gap of 100 bp
* 9337 10088: contig of 752 bp in length
* 10089 10188: gap of 100 bp
* 10189 10928: contig of 740 bp in length
* 10929 11028: gap of 100 bp
* 11029 11780: contig of 752 bp in length
* 11781 11880: gap of 100 bp
* 11881 12632: contig of 752 bp in length
* 12633 12732: gap of 100 bp
* 12733 13476: contig of 744 bp in length
* 13477 13576: gap of 100 bp
* 13577 14335: contig of 759 bp in length
* 14336 14435: gap of 100 bp
* 14436 15194: contig of 759 bp in length
* 15195 15294: gap of 100 bp
* 15295 16065: contig of 771 bp in length
* 16066 16165: gap of 100 bp
* 16166 16924: contig of 759 bp in length
* 16925 17024: gap of 100 bp
* 17025 17783: contig of 759 bp in length
* 17784 17883: gap of 100 bp
* 17884 18636: contig of 753 bp in length
* 18637 18736: gap of 100 bp
* 18737 19485: contig of 749 bp in length
* 19486 19585: gap of 100 bp
* 19586 20342: contig of 757 bp in length
* 20343 20442: gap of 100 bp
* 20443 21209: contig of 767 bp in length
* 21210 21309: gap of 100 bp
* 21310 22086: contig of 777 bp in length
* 22087 22186: gap of 100 bp
* 22187 22950: contig of 764 bp in length
* 22951 23050: gap of 100 bp
* 23051 23802: contig of 752 bp in length
* 23803 23902: gap of 100 bp
* 23903 24649: contig of 747 bp in length
* 24650 24749: gap of 100 bp
* 24750 25507: contig of 758 bp in length
* 25508 25607: gap of 100 bp
* 25608 26364: contig of 757 bp in length
* 26365 26464: gap of 100 bp
* 26465 27221: contig of 757 bp in length
* 27222 27321: gap of 100 bp
* 27322 28089: contig of 768 bp in length
* 28090 28189: gap of 100 bp
* 28190 28968: contig of 779 bp in length
* 28969 29068: gap of 100 bp
* 29069 29837: contig of 769 bp in length
* 29838 29937: gap of 100 bp
* 29938 30679: contig of 742 bp in length
* 30680 30779: gap of 100 bp
* 30780 31511: contig of 732 bp in length
* 31512 31611: gap of 100 bp
* 31612 32390: contig of 779 bp in length
* 32391 32490: gap of 100 bp
* 32491 33251: contig of 761 bp in length
* 33252 33351: gap of 100 bp
* 33352 34098: contig of 747 bp in length
* 34099 34198: gap of 100 bp
* 34199 34942: contig of 744 bp in length
* 34943 35042: gap of 100 bp
* 35043 35785: contig of 743 bp in length

* 35786 35885: gap of 100 bp
* 35886 36646: contig of 761 bp in length
* 36647 36746: gap of 100 bp
* 36747 37500: contig of 754 bp in length
* 37501 37600: gap of 100 bp
* 37601 38371: contig of 771 bp in length
* 38372 38471: gap of 100 bp
* 38472 39240: contig of 769 bp in length
* 39241 39340: gap of 100 bp
* 39341 40097: contig of 757 bp in length
* 40098 40197: gap of 100 bp
* 40198 40919: contig of 722 bp in length
* 40920 41019: gap of 100 bp
* 41020 41767: contig of 748 bp in length
* 41768 41867: gap of 100 bp
* 41868 42623: contig of 756 bp in length
* 42624 42723: gap of 100 bp
* 42724 43493: contig of 770 bp in length
* 43494 43593: gap of 100 bp
* 43594 44345: contig of 752 bp in length
* 44346 44445: gap of 100 bp
* 44446 45198: contig of 753 bp in length
* 45199 45298: gap of 100 bp
* 45299 46043: contig of 745 bp in length
* 46044 46143: gap of 100 bp
* 46144 46914: contig of 771 bp in length
* 46915 47014: gap of 100 bp
* 47015 47789: contig of 775 bp in length
* 47790 47889: gap of 100 bp
* 47890 48652: contig of 763 bp in length
* 48653 48752: gap of 100 bp
* 48753 49504: contig of 752 bp in length
* 49505 49604: gap of 100 bp
* 49605 50358: contig of 754 bp in length
* 50359 50458: gap of 100 bp
* 50459 51226: contig of 768 bp in length
* 51227 51326: gap of 100 bp
* 51327 52087: contig of 761 bp in length
* 52088 52187: gap of 100 bp
* 52188 52948: contig of 761 bp in length
* 52949 53048: gap of 100 bp
* 53049 53824: contig of 776 bp in length
* 53825 53924: gap of 100 bp
* 53925 54755: contig of 831 bp in length
* 54756 54855: gap of 100 bp
* 54856 55699: contig of 844 bp in length
* 55700 55799: gap of 100 bp
* 55800 56678: contig of 879 bp in length
* 56679 56778: gap of 100 bp
* 56779 57612: contig of 834 bp in length
* 57613 57712: gap of 100 bp
* 57713 58521: contig of 809 bp in length
* 58522 58621: gap of 100 bp
* 58622 59446: contig of 825 bp in length

Alignment Scores:

Pred. No.: 8.77e+03 Length: 132446
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x AC024999 (1-132446)

Qy 1 ValLeuGlyLeuGlyGlnPheCys 9
|||
Db 51454 GTTCTGGTGGCTGGCCTGTTCTGC 51480
|||

Search completed: February 18, 2005, 05:26:00
Job time : 1503.08 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2005, 21:47:40 ; Search time 160.74 Seconds
(without alignments)
331.452 Million cell updates/sec

Title: US-10-014-101B-40
Perfect score: 50
Sequence: 1 VLGGGLGQFC 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US10014101/runat_16022005_075845_7925/app_query.fasta_1.796
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101_@CGN_1_1_701_@runat_16022005_075845_7925 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	90.0	65047	11 ACN44020	Acn44020 Mouse gen
2	44	88.0	1509	2 AAQ64910	Aaq64910 Thermus t
3	43	86.0	503	12 ACH75978	Ach75978 Human gen
4	43	86.0	789	12 ACH89659	Ach89659 Human gen
5	43	86.0	5849	6 ABK17335	Abk17335 Human Rb-

C	6	43	86.0	5868	2	AAT18020	Aat18020 Human RIZ
C	7	43	86.0	5868	3	AAA60123	Aaa60123 Human RIZ
C	8	43	86.0	5868	3	AAA60104	Aaa60104 Human RIZ
C	9	43	86.0	5868	3	AAA60124	Aaa60124 Human mut
C	10	43	86.0	5868	6	AAS18781	Aas18781 DNA seque
C	11	43	86.0	5868	9	ACA62689	Aca62689 Human ret
C	12	43	86.0	5868	10	ADE84612	Ade84612 Human ret
C	13	43	86.0	6113	6	ABL33822	Ab133822 Human imm
C	14	43	86.0	6436	6	ABL32681	Ab132681 Human imm
C	15	43	86.0	6704	10	ADF81616	Adf81616 Leukaemia
C	16	43	86.0	7603	6	ABL32308	Ab132308 Human imm
C	17	43	86.0	7603	6	ABL54329	Ab154329 Chemicall
C	18	43	86.0	9504	6	ABK28407	Abk28407 DNA trans
C	19	43	86.0	254087	11	ACN43996	Acn43996 Mouse gen
C	20	42	84.0	531	4	ABL11263	Ab111263 Drosophil
C	21	42	84.0	706	2	ADR02181	Adr02181 A. gossyp
C	22	42	84.0	2262	12	ADQ67514	Adq67514 Novel hum
C	23	42	84.0	2531	4	ABL11262	Ab111262 Drosophil
C	24	42	84.0	7329	4	AAS46674	Aas46674 Tumour su
C	25	42	84.0	12374	10	ADE56064	Ade56064 Human gen
C	26	42	84.0	12374	10	ADD46830	Add46830 Human gen
C	27	42	84.0	13321	4	AAS46421	Aas46421 Tumour su
C	28	41	82.0	255	5	AH82100	Aah82100 Rat diffe
C	29	41	82.0	321	6	ABN23853	Abn23853 Human ORF
C	30	41	82.0	503	3	AAC36788	Aac36788 Arabidops
C	31	41	82.0	537	8	ACA40032	Aca40032 Prokaryot
C	32	41	82.0	552	10	ADH61274	Adh61274 Soybean c
C	33	41	82.0	566	10	ADH61273	Adh61273 Soybean c
C	34	41	82.0	582	10	ADH61277	Adh61277 Soybean c
C	35	41	82.0	635	10	ADH61275	Adh61275 Soybean c
C	36	41	82.0	1088	4	AAH34132	Aah34132 Human col
C	37	41	82.0	1234	6	ABQ34200	Abq34200 Oligonucl
C	38	41	82.0	1234	6	ABQ34201	Abq34201 Oligonucl
C	39	41	82.0	1296	4	AAS51508	Aas51508 Pseudomon
C	40	41	82.0	1296	8	ACA19484	Aca19484 Prokaryot
C	41	41	82.0	1296	11	ABD05092	Abd05092 Pseudomon
C	42	41	82.0	1368	11	ABD05209	Abd05209 Pseudomon
C	43	41	82.0	1506	6	ABK28625	Abk28625 cDNA enco
C	44	41	82.0	1506	9	ACC85294	Acc85294 Arabidops
C	45	41	82.0	1506	10	ADH61267	Adh61267 Arabidops

ALIGNMENTS

RESULT 1
ACN44020
ID ACN44020 standard; DNA; 65047 BP.
AC ACN44020;
XX ACN44020;
DT 18-NOV-2004 (first entry)
XX Mouse genomic sequence mCG12746.
DE Mouse genomic sequence mCG12746.
XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
KW Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
XX Mus musculus.
OS Mus musculus.
XX WO2003073826-A2.
PN WO2003073826-A2.
XX 12-SEP-2003.
PD 12-SEP-2003.
XX 28-FEB-2003; 2003WO-US006235.
PF 28-FEB-2003; 2003WO-US006235.
XX 01-MAR-2002; 2002US-00087192.
PR 01-MAR-2002; 2002US-00087192.
XX (SAGR-) SAGRES DISCOVERY.
PA (SAGR-) SAGRES DISCOVERY.
XX Morris DW;
PI Morris DW;
XX Aaq64910 Thermus t
DR Ach75978 Human gen
XX Ach89659 Human gen
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma

PT comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 259; Opp; English.

PS The present invention relates to novel DNA and protein sequences which

XX are associated with carcinomas. The sequences are useful for: (i) for

CC screening drug candidates; (ii) for screening of bioactive agent capable

CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of

CC a bioactive agent capable of modulating the activity of CAP; (iv) for

CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing

CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating

CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;

CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for

CC determining Carcinoma Associated (CA) gene copy number. In addition, the

CC CA genes are useful as DNA vaccines and the CAP are useful as markers of

CC carcinoma including lymphoma. The present sequence is one such CA coding

CC sequence. Note: This patent is an equivalent to basic patent

CC US2002182586A1, for which no sequence data was published

XX

SQ Sequence 65047 BP; 15178 A; 14282 C; 14920 G; 17577 T; 0 U; 3090 Other;

Alignment Scores:

Pred. No.:	7.53e+03	Length:	65047
Score:	45.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	90.00%	Indels:	0
DB:	11	Gaps:	0

US-10-014-101B-40 (1-9) x ACN44020 (1-65047)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 36758 GTTCTTGGAGTTTGGGGTCCCTTTGT 36784

RESULT 2

AAQ64910/c

ID AAQ64910 standard; DNA; 1509 BP.

XX

AC AAQ64910;

XX

16-OCT-2003 (revised)

DT 10-JAN-1995 (first entry)

XX

Thermus thermophilus carotenoid biosynthesis gene.

DE

XX Carotenoid biosynthesis; food colourant; anticancer agent; antioxidant;

KW recombinant production; ds.

KW

XX Thermus thermophilus; (strain HB27).

OS

XX Key Location/Qualifiers

FH 60..1103

FT /*tag= a

FT /function= "carotenoid_biosynthesis"

XX

PN JP06098774-A.

XX

12-APR-1994.

PD

XX 25-SEP-1992; 92JP-00256580.

PF

XX 25-SEP-1992; 92JP-00256580.

PR

XX (MITP) MITSUBISHI PETROCHEMICAL CO LTD.

PA

XX WPI; 1994-155923/19.

DR P-PSDB; AAR54865.

DR

XX Carotenoid biosynthesis gene from Thermus - and transformed Thermus hosts

PT to enhance carotenoid prodn. for use as food colourant, anticancer agent

PT etc.

XX

PS Claim 4; Page 8-9; 12pp; Japanese.

XX

CC DNA was isolated from T.thermophilus HB27, digested with HindIII and

CC inserted into plasmid pYK134. The plasmids were used to transform T.

CC thermophilus HB27 hosts and fragments of interest were selected by growth

CC of orange colonies on kanamycin-contg. medium. Recombinant production of

CC carotenoids (useful as antioxidants, food colourants, anticancer agents,

CC etc.) can be enhanced using the transformed hosts. (Updated on 16-OCT-

CC 2003 to standardise OS field)

XX

SQ Sequence 1509 BP; 208 A; 560 C; 537 G; 204 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	188	Length:	1509
Score:	44.00	Matches:	7
Percent Similarity:	88.89%	Conservative:	1
Best Local Similarity:	77.78%	Mismatches:	1
Query Match:	88.00%	Indels:	0
DB:	2	Gaps:	0

US-10-014-101B-40 (1-9) x AAQ64910 (1-1509)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 61 ATTCTAGCGCGCCTCGGGACTTTTGC 35

RESULT 3

ACH75978

ID ACH75978 standard; DNA; 503 BP.

XX

AC ACH75978;

XX

29-JUL-2004 (first entry)

DT

XX Human genome derived single exon probe #9173.

DE

XX Human; probe; ss; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

KW

XX Homo sapiens.

OS

XX US2003194704-A1.

PN

XX 16-OCT-2003.

PD

XX 03-APR-2002; 2002US-00029386.

PF

XX 03-APR-2002; 2002US-00029386.

PR

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX

PI Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

DR

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX

PS Claim 15; SEQ ID NO 9173; 80pp; English.

XX

CC The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above- mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subcription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising gross
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX SQ Sequence 503 BP; 101 A; 124 C; 121 G; 157 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 86.4 Length: 503
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-40 (1-9) x ACH75978 (1-503)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
| | | | | | | | | | | | | | | | | | | | | |
Db 4 GTTCTGGTGGCTGGCGCTGTTCTGC 30

RESULT 4
ACH89659
ID ACH89659 standard; DNA; 789 BP.
XX ACH89659;
AC ACH89659;
XX ACH89659;
DT 29-JUL-2004 (first entry)
XX Human genome derived single exon probe #22854.
DE Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
KW Homo sapiens.

OS US2003194704-A1.
XX 16-OCT-2003.
XX 03-APR-2002; 2002US-00029386.
XX 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

XX Claim 1; SEQ ID NO 22854; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above- mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subcription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising gross
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX SQ Sequence 789 BP; 187 A; 176 C; 172 G; 254 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 141 Length: 789
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-40 (1-9) x ACH89659 (1-789)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
| | | | | | | | | | | | | | | | | | | | | |
Db 468 GTTCTGGTGGCTGGCGCTGTTCTGC 494

RESULT 5
ABK17335/c
ID ABK17335 standard; cDNA; 5849 BP.

XX ABK17335;
AC ABK17335;
XX 26-MAR-2002 (first entry)
XX Human Rb-interacting zinc finger (RIZ) cDNA.

XX Rat; human; retinoblastoma protein-interacting zinc finger protein; RIZ;
KW ss; PRDI-BF1; human positive regulatory domain I-binding factor 1; EVI-1;
KW human ecotropic viral integration site-1 myeloid transforming gene; Rb;

KW Caenorhabditis elegans; egl-43; retinoblastoma protein; cardiac muscle; cell proliferation; cancer; cell proliferation; neural cell; paralysis; neurodegenerative disease; Parkinson's disease; Huntington's disease; Alzheimer's disease; motor neuron disorder; PCR primer; mouse; E1A; mutagenesis primer.

OS Homo sapiens.

XX US6323335-B1.

XX 27-NOV-2001.

PF 01-JUN-2000; 2000US-00586472.

XX 18-AUG-1994; 94US-00292683.

PR 06-MAR-1995; 95US-00399411.

PR 18-AUG-1995; 95US-00516859.

PR 17-MAR-2000; 2000US-00528706.

XX (HUAN/) HUANG S.

XX Huang S;

PI WPI; 2002-096600/13.

XX P-PSDB; AAU80804.

DR Novel nucleic acid molecule comprises the code for a conserved domain of retinoblastoma protein-interacting zinc finger protein, positive regulatory domain I-binding factor involved in regulating gene transcription.

XX Example 1; Fig 9A; 93pp; English.

XX The invention relates to a nucleic acid molecule encoding a PR domain peptide present in human and rat retinoblastoma protein-interacting zinc finger protein (RIZ); PRDI-BF1 (human positive regulatory domain I-binding factor 1), EVI-1 (human ecotropic viral integration site-1 myeloid transforming gene product) or Caenorhabditis elegans egl-43 gene product. The DNA of the invention is involved in regulating transcription of a target gene. RIZ acts as a cell-differentiation factor and modulates a function of a cell by binding to retinoblastoma (Rb) protein, which is involved in regulating cell proliferation in various human diseases or conditions, e.g. cancer. RIZ regulates the growth of normal adult cardiac muscle cells and prevents proliferation of surviving cells following cardiac muscle cell death. RIZ is expressed in neural cells. This is useful for healing after injury of neural tissue and for treating neurodegenerative diseases such as Parkinson's, Huntington's or Alzheimer's disease and paralysis, or motor neuron disorders through induced or decreased proliferation of neural cells. The PR domain or RIZ active fragment containing a PR domain is useful as a probe to identify transcription factors or oncogenic proteins in a cell that bind the PR domain. Sequences ABK17334-ABK17353 represent DNA molecules and primers of the invention

XX Sequence 5849 BP; 1693 A; 1468 C; 1347 G; 1341 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.27e+03	Length:	5849
Score:	43.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	86.00%	Indels:	0
DB:	6	Gaps:	0

US-10-014-101B-40 (1-9) x ABK17335 (1-5849)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||

Db 1727 GTTCTGGGTGGCTGGGCTGTTCTGC 1701

RESULT 6
AAT18020/c
ID AAT18020 standard; cDNA; 5868 BP.

XX AAT18020;

AC 19-MAY-1996 (first entry)

DT XX

DE Human RIZ allele D283 cDNA.

XX Retinoblastoma protein-interacting zinc finger; RIZ; cell proliferation; tumour; cancer; neuroblastoma; melanoma; diagnosis; gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 121. .5280

FT /*tag= a

FT repeat_region 952. .981

FT /*tag= b

FT /note= "triplet repeat region is (GAA)5(GAT)5 in the D283 allele and (GAA)6(GAT)4 in the E283 allele"

FT 969

FT /*tag= c

FT /note= "base 969 is t in the D283 allele and a in the E283 allele"

XX WO9606168-A2.

PN 29-FEB-1996.

PD 18-AUG-1995; 95WO-US010574.

XX 18-AUG-1994; 94US-00292683.

PR 06-MAR-1995; 95US-00399411.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

PA Huang S;

PI WPI; 1996-151371/15.

XX P-PSDB; AAR92100.

DR Nucleic acid encoding mammalian retinoblastoma protein-interacting zinc finger - used to identify cell proliferation modulating agents for treatment of tumours, esp. neuroblastoma and melanoma, also used for cancer diagnosis.

XX Claim 4; Fig 9A; 142pp; English.

PS A complete human retinoblastoma (Rb) protein-interacting zinc finger (RIZ) cDNA sequence (AAT18020) was cloned from human foetal brain cDNA using rat RIZ cDNA (see AAT18023) coding region as probe. The human RIZ genomic DNA has 8 exons and is located on chromosome 1p36. The RIZ D283 allele occurs 2 times more frequently in the human population than another identified RIZ allele, E283. Clones (AAT18021-22) encoding 2 alternative 5'-termini of human RIZ were also obtd. RIZ-encoding sequences are used for production of RIZ or its active fragments by recombinant DNA methods, in the diagnosis of disorders associated with abnormal levels of RIZ expression, or may be incorporated into e.g. viral vectors for use in gene therapy

XX Sequence 5868 BP; 1697 A; 1475 C; 1354 G; 1342 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.27e+03	Length:	5868
Score:	43.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	86.00%	Indels:	0
DB:	2	Gaps:	0

US-10-014-101B-40 (1-9) x AAT18020 (1-5868)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||

Db 1728 GTTCTGGTGGCTGGCCTGTTCTGC 1702

RESULT 7

AAA60123/c

ID AAA60123 standard; DNA; 5868 BP.

XX AAA60123;

AC AAA60123;

XX 17-JAN-2001 (first entry)

DT 17-JAN-2001 (first entry)

XX Human RIZ allele E283 coding sequence.

DE Human; Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;

XX cell proliferation; cell differentiation; tissue repair;

KW transcription regulator; breast cancer; gene therapy; melanoma;

KW neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease;

KW Alzheimer's disease; paralysis; motor neurone disorder; chromosome 1p36;

KW ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT CDS

FT Location/Qualifiers

FT 121..5280

FT /*tag= a

FT /product= "Human RIZ protein"

FT repeat_region

FT 952..981

FT /*tag= b

FT /rpt_type= TANDEM

FT replace(969,T)

FT /*tag= C

XX allele

XX US6069231-A.

XX 30-MAY-2000.

XX 18-AUG-1995; 95US-00516859.

XX 18-AUG-1994; 94US-00292683.

PR 06-MAR-1995; 95US-00399411.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Huang S;

XX WPI; 2000-410879/35.

DR P-PSDB; AAB12113.

XX New PR domain peptides comprising amino acid sequences from, for example

PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for

PT regulating gene transcription and controlling cell proliferation and

PT differentiation.

XX Disclosure; Page; 91pp; English.

XX The present sequence is the human retinoblastoma (Rb)-interacting zinc

CC finger (RIZ) protein allele E283 coding sequence. RIZ is a nuclear

CC phosphoprotein that acts as a cell differentiation factor. RIZ can

CC modulate cell growth by binding to Rb protein, which is involved in

CC regulating cell proliferation. In addition, RIZ can act to regulate

CC transcription. RIZ functions to maintain cells in the G1 phase of the

CC cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ

CC protein is a PR domain protein and is present primarily in the cell

CC nucleus. RIZ gene mutations may be implicated in various cancers such as

CC melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene

CC may be used in gene therapy for these disorders. Since RIZ protein is

CC implicated in cell cycle arrest, inhibition of RIZ activity may be useful

CC in neurodegenerative disorder therapy e.g. for Parkinson's, Huntingdon's

CC or Alzheimer's disease, paralysis or motor neurone disorders, or cardiac

CC disorder therapy e.g. heart disease where the ability to induce neural/

CC cardiac tissue proliferation would be useful. The human RIZ gene is

CC located on chromosome 1p36. The RIZ D283 allele is thought to occur two

CC times more frequently in the human population than the RIZ E283 allele

CC (AAA60104 and AAB12029)

XX Sequence 5868 BP; 1698 A; 1474 C; 1353 G; 1343 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 1.27e+03 Length: 5868

Score: 43.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 86.00% Indels: 0

DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x AAA60123 (1-5868)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 1728 GTTCTGGTGGCCTGGCCTGTTCTGC 1702

RESULT 8

AAA60104/c

ID AAA60104 standard; DNA; 5868 BP.

XX AAA60104;

AC AAA60104;

XX 17-JAN-2001 (first entry)

DE Human RIZ allele D283 coding sequence.

XX Human; Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;

KW cell proliferation; cell differentiation; tissue repair;

KW transcription regulator; breast cancer; gene therapy; melanoma;

KW neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease;

KW Alzheimer's disease; paralysis; motor neurone disorder; chromosome 1p36;

KW ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT CDS

FT Location/Qualifiers

FT 121..5280

FT /*tag= a

FT /product= "Human RIZ protein"

FT repeat_region

FT 952..981

FT /*tag= b

FT /rpt_type= TANDEM

FT replace(969,A)

FT /*tag= C

XX US6069231-A.

XX 30-MAY-2000.

XX 18-AUG-1995; 95US-00516859.

XX 18-AUG-1994; 94US-00292683.

PR 06-MAR-1995; 95US-00399411.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Huang S;

XX WPI; 2000-410879/35.

DR P-PSDB; AAB12029.

XX New PR domain peptides comprising amino acid sequences from, for example

PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for

PT regulating gene transcription and controlling cell proliferation and

PT differentiation.

XX Example 1; Fig 9; 91pp; English.

PS The present sequence is the human retinoblastoma (Rb)-interacting zinc

CC finger (RIZ) protein allele D283 coding sequence. RIZ is a nuclear

CC phosphoprotein that acts as a cell differentiation factor. RIZ can

CC modulate cell growth by binding to Rb protein, which is involved in

CC regulating cell proliferation. In addition, RIZ can act to regulate
CC transcription. RIZ functions to maintain cells in the G1 phase of the
CC cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ
CC protein is a PR domain protein and is present primarily in the cell
CC nucleus. RIZ gene mutations may be implicated in various cancers such as
CC melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene
CC may be used in gene therapy for these disorders. Since RIZ protein is
CC implicated in cell cycle arrest, inhibition of RIZ activity may be useful
CC in neurodegenerative disorder therapy e.g. for Parkinson's, Huntington's
CC or Alzheimer's disease, paralysis or motor neurone disorders, or cardiac
CC disorder therapy e.g. heart disease where the ability to induce neural/
CC cardiac tissue proliferation would be useful. The human RIZ gene is
CC located on chromosome 1p36. The RIZ D283 allele is thought to occur two
CC times more frequently in the human population than the RIZ E283 allele
CC (AAA60123 and AAB12113)

XX
SQ Sequence 5868 BP; 1697 A; 1474 C; 1353 G; 1344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e+03 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x AAA60104 (1-5868)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 1728 GTTCTGGGTGGCCTGGCCTGTTCTGC 1702

RESULT 9
AAA60124/c
ID AAA60124 standard; DNA; 5868 BP.

XX
AC AAA60124;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human mutant RIZ allele D283 coding sequence.

XX Human; Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;
KW cell proliferation; cell differentiation; tissue repair;
KW transcription regulator; breast cancer; gene therapy; melanoma;
KW neuroblastoma; leukaemia; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; paralysis; motor neurone disorder; chromosome 1p36;
KW mutation; ds.

XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 121..5280
FT /*tag= a
FT /product= "Human RIZ protein"
FT mutation replace(437,G)
FT /*tag= b
FT repeat_region 952..981
FT /*tag= c
FT allele /rpt_type= TANDEM
FT replace(969,A)
FT /*tag= d

XX US6069231-A.
XX
PD 30-MAY-2000.
XX
PF 18-AUG-1995; 95US-00516859.
XX
PR 18-AUG-1994; 94US-00292683.
PR 06-MAR-1995; 95US-00399411.
XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Huang S;
XX
DR WPI; 2000-410879/35.
DR P-PSDB; AAB12114.
XX

PT New PR domain peptides comprising amino acid sequences from, for example
PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for
PT regulating gene transcription and controlling cell proliferation and
PT differentiation.

XX Disclosure; Page; 91pp; English.

XX
CC The present sequence is a mutant human retinoblastoma (Rb)-interacting
CC zinc finger (RIZ) protein allele D283 coding sequence. RIZ is a nuclear
CC phosphoprotein that acts as a cell differentiation factor. RIZ can
CC modulate cell growth by binding to Rb protein, which is involved in
CC regulating cell proliferation. In addition, RIZ can act to regulate
CC transcription. RIZ functions to maintain cells in the G1 phase of the
CC cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ
CC protein is a PR domain protein and is present primarily in the cell
CC nucleus. RIZ gene mutations may be implicated in various cancers such as
CC melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene
CC may be used in gene therapy for these disorders. Since RIZ protein is
CC implicated in cell cycle arrest, inhibition of RIZ activity may be useful
CC in neurodegenerative disorder therapy e.g. for Parkinson's, Huntington's
CC or Alzheimer's disease, paralysis or motor neurone disorders, or cardiac
CC disorder therapy e.g. heart disease where the ability to induce neural/
CC cardiac tissue proliferation would be useful. The human RIZ gene is
CC located on chromosome 1p36. The RIZ D283 allele is thought to occur two
CC times more frequently in the human population than the RIZ E283 allele
CC (AAA60123 and AAB12113). Note: the present sequence is not shown in the
CC specification but is derived from the human RIZ allele D283 sequence
CC given in Figure 9 (see AAA60104)

XX
SQ Sequence 5868 BP; 1698 A; 1474 C; 1352 G; 1344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e+03 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x AAA60124 (1-5868)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 1728 GTTCTGGGTGGCCTGGCCTGTTCTGC 1702

RESULT 10
AAS18781/c
ID AAS18781 standard; DNA; 5868 BP.
XX
AC AAS18781;
XX
DT 26-MAR-2002 (first entry)
XX
DE DNA sequence encoding human RIZ1 (hRIZ1).

XX
KW Suppression of tumour growth; MSI positive tumour; hRIZ1; human;
KW retinoblastoma protein-interacting zinc finger; cancer; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 121..5280
FT /*tag= a
FT /product= "hRIZ1"
XX
PN CN1313130-A.

XX 19-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001CN-00109921.
PF
XX
XX 23-MAR-2001; 2001CN-00109921.
PR
XX
XX (HUAN/) HUANG S.
PA
XX
XX Huang S;
PI
XX
XX WPI; 2002-042166/06.
DR
XX P-PSDB; AAU10788.
DR
XX Application of RIZ gene in detecting and treating tumor showing MSI
PT positive.
PT
XX
XX Disclosure; Page 29-36 (Disclosure); 54pp; Chinese.
PS
XX
XX The present invention relates to a method for suppressing growth of
CC tumours showing MSI positive. The DNA sequence of coded functional RIZ1
CC (retinoblastoma protein-interacting zinc finger) polypeptide is
CC transferred to the MSI positive tumour and the RIZ1 protein which can
CC suppress growth of the tumour is expressed in the tumour. A method for
CC determining the MSI state of a tumour is also described. The method
CC features that the number of adenines in polyadenine in the RIZ1 gene is
CC detected to determine if the tumour is MSI positive. When the number of
CC adenines is abnormal, the tumour is MSI positive. The invention is useful
CC in the treatment of cancers. The present sequence encodes for human RIZ1
CC (hRIZ1)
XX
SQ Sequence 5868 BP; 1697 A; 1474 C; 1353 G; 1344 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.27e+03 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-40 (1-9) x AAS18781 (1-5868)
QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1728 GTTCTGGTGGCCTGGGCGCTGTCTGC 1702
RESULT 11
ACA62689/c
ID ACA62689 standard; DNA; 5868 BP.
XX
XX ACA62689;
AC
XX 20-AUG-2003 (first entry)
DT
XX Human retinoblastoma protein interacting zinc finger gene, RIZ1, DNA.
DE
XX Human; gene; RIZ1; microsatellite instability; MSI; tumour; apoptosis;
KW retinoblastoma protein interacting zinc finger gene; colorectal tumour;
KW endometrial tumour; hereditary nonpolyposis colon carcinoma; ds;
KW gastric tumour.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 121..5280
CDS /*tag= a
FT /product= "RIZ1"
FT replace(969,A)
FT /*tag= b
XX
XX US2003032606-A1.
PN
XX

PD 13-FEB-2003.
XX
XX 17-DEC-2001; 2001US-00024450.
PF
XX
XX 19-DEC-2000; 2000US-0256582P.
PR
XX
XX (HUAN/) HUANG S.
PA
XX (CHAD/) CHADWICK R B.
PA
XX Huang S, Chadwick RB;
PI
XX
XX WPI; 2003-492075/46.
DR
XX P-PSDB; ABU62110, ABU62116.
DR
XX Inhibiting growth of microsatellite instability-positive tumor, by
PT introducing a nucleic acid molecule encoding a retinoblastoma protein-
PT interacting zinc finger gene-1 polypeptide into the tumor.
PT
XX
XX Disclosure; Page 20-26; 41pp; English.
PS
XX The invention relates to a method of inhibiting growth of a
CC microsatellite instability (MSI)-positive tumour, which involves
CC introducing into the tumour a nucleic acid molecule encoding a
CC retinoblastoma protein-interacting zinc finger gene (RIZ)-1 polypeptide
CC and expressing the polypeptide in the tumour in an effective amount to
CC inhibit growth of the tumour. The method is useful for inhibiting growth
CC of a microsatellite instability (MSI)-positive tumour. The tumour
CC contains cells having an abnormal number of adenine nucleotides in a
CC RIZ poly(A) tract. The MSI-positive tumour is colorectal tumour, gastric
CC tumour, endometrial tumour or hereditary nonpolyposis colon carcinoma.
CC Also disclosed is a method for determining MSI status of the tumour. Both
CC methods are useful for detecting and treating MSI(+) tumours and for
CC inducing apoptotic cell killing both in vitro and in vivo. The present
CC sequence represents the human retinoblastoma protein interacting zinc
CC finger gene, RIZ1, DNA
XX
SQ Sequence 5868 BP; 1697 A; 1474 C; 1353 G; 1344 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.27e+03 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 9 Gaps: 0
US-10-014-101B-40 (1-9) x ACA62689 (1-5868)
QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1728 GTTCTGGTGGCCTGGGCGCTGTCTGC 1702
RESULT 12
ADE84612/c
ID ADE84612 standard; cDNA; 5868 BP.
XX
XX ADE84612;
AC
XX 29-JAN-2004 (first entry)
DT
XX Human retinoblastoma protein-interacting zinc finger (RIZ) protein cDNA.
DE
XX
XX cytosstatic; tumor; gene therapy;
KW retinoblastoma protein-interacting zinc protein; RIZ; neuroblastoma;
KW melanoma; cardiac cell growth inducer; neuronal cell growth inducer;
KW human; gene; ss.
XX
XX Homo sapiens.
OS
XX US6468985-B1.
PN
XX 22-OCT-2002.
PD
XX

PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
DR
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 654; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 6436 BP; 1509 A; 261 C; 1477 G; 3189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.4e+03 Length: 6436
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABL32681 (1-6436)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 5764 GTTTGGTGGGTAGGTGTTTTTTC 5790

RESULT 15
ADP81616/c
ID ADF81616 standard; DNA; 6704 BP.
XX
AC ADF81616;
XX
DT 26-FEB-2004 (first entry)
XX
DE Leukaemia-related DNA sequence #2172.
XX
KW Cytostatic; Gene therapy; leukaemia; ss.
XX
OS Unidentified.
XX
PN WO2003039443-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-EP012303.
XX
PR 05-NOV-2001; 2001EP-00126244.
PR 30-APR-2002; 2002EP-00009758.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
XX
PI Haerlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
PI Eils R, Brors B, Mergenthaler S;
XX
DR WPI; 2003-505037/47.
XX
PT Determining the subtype of leukemia cells and whether a patient sample
PT contains leukemia cells or other cells, useful for treating leukemia,
PT comprises determining the expression profile of a group of markers in a
PT patient sample.

XX Disclosure; SEQ ID NO 2172; 2938pp; English.
PS
XX
CC The present invention relates to a method (M1) for determining the
CC subtype of leukaemia cells and whether a patient sample contains
CC leukaemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukaemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukaemia.
XX
SQ Sequence 6704 BP; 1992 A; 1530 C; 1451 G; 1696 T; 0 U; 35 Other;

Alignment Scores:
Pred. No.: 1.47e+03 Length: 6704
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADF81616 (1-6704)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1476 GTTCTGGTGGCCTGGGCCCTGTTCTGC 1450

RESULT 16
ABL32308
ID ABL32308 standard; DNA; 7603 BP.
XX
AC ABL32308;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 281.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; anti-anaemic; cytosine methylation; antiasthmatic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 281; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 7603 BP; 1892 A; 88 C; 1729 G; 3894 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.69e+03 Length: 7603
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABL32308 (1-7603)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 334 GTTTGGGTGGGTAGGTGTTTGT 360

RESULT 17
ABL54329
ID ABL54329 standard; DNA; 7603 BP.
XX
AC ABL54329;
XX
DT 29-JUL-2002 (first entry)
XX
DE Chemically treated apoptosis gene #15.
XX
KW Apoptosis; HIV; Bloom syndrome; cardiopathy; neurodegenerative disorder;
KW Herpes simplex virus; renal ischaemia; amyotrophic lateral sclerosis;
KW cancer; ds.
XX
OS Unidentified.
XX
PN WO200177164-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-EP003969.
XX
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-017444/02.
XX
PT Chemically modified sequences of genes associated with apoptosis are
PT useful to determine methylation patterns of genomic DNA samples for
PT diagnosis of associated diseases such as cancer.
XX
PS Claim 1; Seq ID #29; 24pp; English.
XX
CC This invention relates to chemically pre-treated DNA of genes associated
CC with apoptosis. The nucleic acids are used to allocate patients for
CC specific therapy for HIV infection, Bloom syndrome, cardiopathy, aging,
CC neurodegenerative disorders, Herpes simplex virus infection, renal
CC ischaemia, amyotrophic lateral sclerosis, solid tumours and cancers. This
CC nucleotide sequence represents a chemically treated apoptosis gene. Even
CC SEQ ID numbers are the complementary DNA strands to the odd SEQ ID
CC numbers. The sequence data for this patent is not represented in the
CC printed specification but is based on information supplied by the
CC European patent office
XX
SQ Sequence 7603 BP; 1892 A; 88 C; 1729 G; 3894 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.69e+03 Length: 7603
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABL54329 (1-7603)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 334 GTTTGGGTGGGTAGGTGTTTGT 360

RESULT 18
ABK28407
ID ABK28407 standard; DNA; 9504 BP.
XX
AC ABK28407;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA transcription associated genomic DNA #141.
XX
KW DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
KW PNA; cytosine methylation state; SNP; retroviral infection; gene; ds;
KW single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
KW viral infection; Sezary syndrome; haematological disorder; tuberculosis;
KW immunological disorder; Werner syndrome; developmental disorder;
KW psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
KW neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease;
KW myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
KW angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
KW polyglutamine disorder; solid tumour.
XX
OS Unidentified.
XX
PN WO200192565-A2.
XX
PD 06-DEC-2001.
XX
PF 06-APR-2001; 2001WO-EP003973.
XX
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-090046/12.
XX
PT New nucleic acids or oligomers, useful for diagnosing or treating
PT diseases associated with DNA transcription, e.g. immunological disorders,
PT Werner syndrome, psoriasis, myocardial infarction, solid tumors or
PT cancer.
XX
PS Claim 1; SEQ ID NO 281; 32pp; English.
XX
CC The invention relates to a nucleic acid, which comprises a segment of the
CC chemically pretreated DNA of genes associated with DNA transcription from
CC one of 346 sequences, and an oligomer, in particular an oligonucleotide
CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
CC to the chemically pretreated DNA of genes associated with DNA
CC transcription. The set of oligomer probes are useful for detecting the
CC cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
CC in a chemically pretreated genomic DNA. The nucleic acids are useful for
CC diagnosing or treating diseases associated with DNA transcription
CC (particularly with the methylation status), e.g. adenosine deaminase
CC deficiency, viral infection, retroviral infection, Sezary syndrome,
CC haematological disorders, immunological disorders, Werner syndrome,
CC tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,

CC neurological disorders, neurodegenerative disorders, Waardenburg
CC syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
CC infarction, hypertension, angiogenesis, erythropoiesis, congenital heart
CC disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours
CC or cancer. Sequences ABK28127-ABK28472 represent DNA transcription
CC associated genomic DNA molecules of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format directly from the European Patent
CC Office

SQ Sequence 9504 BP; 2528 A; 138 C; 1853 G; 4985 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.15e+03 Length: 9504
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABK28407 (1-9504)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 6626 GTTTGGTGGGTAGGTGTTTTTCT 6652

RESULT 19
ACN43996
ID ACN43996 standard; DNA; 254087 BP.
XX
AC ACN43996;
XX
DT 18-NOV-2004 (first entry)
DE Mouse genomic sequence MCG12572.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
OS Mus musculus.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.

PS Claim 1; SEQ ID NO 223; Opp; English.
XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published

XX
SQ Sequence 254087 BP; 65528 A; 53970 C; 55490 G; 73068 T; 0 U; 6031 Other;
Alignment Scores:
Pred. No.: 7.83e+04 Length: 254087
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-40 (1-9) x ACN43996 (1-254087)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 241873 GTACTGGAGGCTTGGGTTGTTTTC 241899

RESULT 20
ABL11263/c
ID ABL11263 standard; cDNA; 531 BP.
XX
AC ABL11263;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28271.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB67160.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28271; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX ,Sequence 531 BP; 140 A; 142 C; 167 G; 82 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 140 Length: 531
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0

DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x ABL11263 (1-531)

QY 3 GlyGlyLeuGlyGlnPheCys 9
|||||

Db 188 GCGGGTTGGGGCAATTCTGC 168

RESULT 21
ADRO2181

ID ADR02181 standard; DNA; 706 BP.

XX

AC ADR02181;

XX

DT 23-SEP-2004 (first entry)

XX

DE A. gossypii genomic DNA PAG1548RP.

XX

KW Filamentous funghi; ds; forensic identification; gene characterisation;

KW intergenomic comparison; chromosome mapping.

XX

OS Eremothecium gossypii.

XX

PN US6239264-B1.

XX

PD 29-MAY-2001.

XX

PF 24-DEC-1997; 97US-00998416.

XX

PR 31-DEC-1996; 97CH-00000016.

XX

PA (SYNG-) SYNGENTA PARTICIPATIONS AG.

XX

PI Philippssen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;

PI Knechtle P, Rebischung C;

XX

DR WPI; 1998-388120/33.

XX

PT New gene for adenylate cyclase from Ashbya gossypii - useful for

PT generating recombinant microorganisms with alteration in gene of cAMP-

PT dependent signalling pathway for increasing production of fine chemicals.

XX

PS Example 3; SEQ ID NO 873; 632pp; English.

XX

CC The invention relates to isolated DNA molecules comprising isolated

CC genomic DNA sequences from the filamentous funghi Ashbya gossypii, the

CC sequences comprising ADR01309, ADR01366, ADR01367, ADR01388, ADR01428,

CC ADR01466; ADR01629, ADR01637, ADR02057, ADR02345 and ADR02369, chosen

CC from 1047 disclosed genomic sequences. Also included is a cloning vector

CC comprising a nucleotide sequence chosen from the above sequences. The

CC novel Ashbya gossypii genomic sequences are useful for forensic

CC identification, gene characterisation, for studying gene organisation by

CC intergenomic comparison (with Saccharomyces cerevisiae), identifying

CC biosynthetic genes for selectable markers, to isolate

CC promoters/terminators/centromeres, chromosome mapping, and in identifying

CC sequences unique to Ashbya gossypii for species identification. The

CC present sequence is an A. gossypii novel genomic sequence of the

invention.

XX

SQ Sequence 706 BP; 138 A; 185 C; 182 G; 201 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	192	Length:	706
Score:	42.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	84.00%	Indels:	0
DB:	2	Gaps:	0

US-10-014-101B-40 (1-9) x ADR02181 (1-706)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||

Db 344 CTGGCGGGTTTGGGCAGTTCTGC 367

RESULT 22
ADQ67514/c

ID ADQ67514 standard; cDNA; 2262 BP.

XX

AC ADQ67514;

XX

DT 07-OCT-2004 (first entry)

XX

DE Novel human cDNA sequence #2487.

XX

KW ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;

KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;

KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

KW cancer.

XX

OS Homo sapiens.

XX

PN EP1440981-A2.

XX

PD 28-JUL-2004.

XX

PF 21-JAN-2004; 2004EP-00001196.

XX

PR 21-JAN-2003; 2003JP-00102206.

PR 09-MAY-2003; 2003JP-00131392.

XX

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX

DR WPI; 2004-535376/52.

DR P-PSDB; ADQ67821.

XX

PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX

PS Claim 1; SEQ ID NO 4675; 2449pp; English.

XX

CC The invention relates to 2495 novel polynucleotides (I) and their encoded

CC polypeptides, sequences hybridizing to these nucleotides, sequences

CC encoding partial polypeptides and sequences having 70% or 90% identity to

CC the nucleotide and protein sequences. The nucleotides and polypeptides

CC are useful as diagnostic markers or therapeutic target for the diseases

CC or morbid states. They are also useful for treating osteoporosis,

CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,

CC dementia and various cancers. This sequence corresponds to a nucleotide

CC sequence of the invention.

XX

SQ Sequence 2262 BP; 595 A; 635 C; 545 G; 487 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	685	Length:	2262
Score:	42.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	84.00%	Indels:	0
DB:	12	Gaps:	0

US-10-014-101B-40 (1-9) x ADQ67514 (1-2262)

QY 3 GlyGlyLeuGlyGlnPheCys 9
|||||

Db 1176 GGAGGACTTGGGCAATTCTGC 1156

RESULT 23
ABL11262/c

ID ABL11262 standard; cDNA; 2531 BP.

XX

AC ABL11262;

XX

```

DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28268.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB67159.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28268; 2lpp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2531 BP; 748 A; 489 C; 587 G; 707 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 775 Length: 2531
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x ABL11262 (1-2531)

Qy 3 GlyGlyLeuGlyGlnPheCys 9
Db 1188 GCGGGTGGGGCAATCTGC 1168

RESULT 24
AAS46674
ID AAS46674 standard; DNA; 7329 BP.
XX
AC AAS46674;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #396.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.

```


XX DE Human gene NM_001372, SEQ ID NO 1903.
XX KW Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
DR GENBANK; NM_001372.
XX PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI)) in a human DNA (shown in Table 2 of the
CC therapy). The sequence presented is a human DNA (shown in Table 2 of the
CC specification) which encodes one of the polypeptides of the invention
CC which is differentially expressed during pain. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 12374 BP; 3200 A; 3172 C; 3279 G; 2723 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.39e+03 Length: 12374
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADE56064 (1-12374)

QY 3 GlyGlyLeuGlyGlnPheCys 9
Db |||||
2821 GGAGGTCTGGGTCACTTCTGC 2841
RESULT 26
ADD46830
ID ADD46830 standard; DNA; 12374 BP.
XX AC ADD46830;
XX DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX DE Human gene NM_001372, SEQ ID NO 12516.
XX KW Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
OS Unidentified.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
DR GENBANK; NM_001372.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Example 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in a human DNA (described in Table 3 of the specification) which encodes one of the polypeptides of the invention which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 12374 BP; 3200 A; 3172 C; 3279 G; 2723 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.39e+03 Length: 12374
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADD46830 (1-12374)

Qy 3 GlyGlyLeuGlyGlnPheCys 9
|||||
Db 2821 GGAGGCTGGGTCAGTTCTGC 2841

RESULT 27
AAS46421
ID AAS46421 standard; DNA; 13321 BP.
XX AC AAS46421;
XX 18-DEC-2001 (first entry)
XX Tumour suppressor gene derived chemically modified sequence #143.
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX Homo sapiens.
OS WO200168912-A2.
XX PN 20-SEP-2001.
XX 15-MAR-2001; 2001WO-EP002955.
XX 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-602752/68.
XX Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX Claim 1; SEQ ID NO 143; 27pp; English.

XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to

CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13321 BP; 2515 A; 580 C; 4121 G; 6105 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.76e+03 Length: 13321
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x AAS46421 (1-13321)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 10259 GTATAGGTGGTGTGCGAGATTGT 10285

RESULT 28
AAH82100/c
ID AAH82100 standard; DNA; 255 BP.
XX AC AAH82100;
XX 21-SEP-2001 (first entry)
XX Rat differential transcription-associated cDNA SEQ ID 609.
KW Differential transcription; human; rat; tumour cell; cytostatic;
KW Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX Rattus sp.
XX WO200157058-A2.
XX 09-AUG-2001.
XX 31-JAN-2001; 2001WO-EP001003.
XX 31-JAN-2000; 2000DE-01004102.
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

PA Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;
XX Grips M, Hellriegel M, Schmitz A, Sers C;
XX WPI; 2001-483415/52.

XX Nucleic acids differentially expressed between tumor and normal cells,
PT useful for diagnosis or therapy of tumors and for screening active
PT agents.
XX Claim 6; Page 529; 579pp; German.

XX This invention describes a nucleic acid (I) with differential expression
CC between tumour and normal cells and which has cytostatic activity. (I)
CC work as modulators of Ras activity by inducing expression of tumour
CC suppressor genes. (I), and polypeptides encoded by them, are useful as
CC targets for diagnosis or therapy and in screening to determine the
CC effects of an active compound (potential pharmaceutical) on a cell line,
CC particularly for diagnosis and treatment of tumors, especially by
CC modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
CC methods) or by modulating the amount and/or location of (I)-encoded
CC polypeptides (by administration of the polypeptide or its activator,
CC antibody (optionally as a conjugate) or inhibitor). The method allows
CC identification of many Class II tumour suppressor genes (i.e. genes that
CC are not primary targets for tumour-initiating mutations). AAH81492-
CC AAH82376 represent the human and rat derived nucleic acid fragments
CC described in the method of the invention

XX SQ Sequence 255 BP; 83 A; 45 C; 77 G; 50 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 96.3 Length: 255
Score: 41.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x AAH82100 (1-255)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 179 CTGGTGGGTGGGCCATTCTGT 156
|||||

RESULT 29
ABN23853/c
ID ABN23853 standard; cDNA; 321 BP.
XX AC ABN23853;
XX

DT 24-JUN-2002 (first entry)

DE Human ORFX polynucleotide sequence SEQ ID NO:16183.

XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.

XX OS Homo sapiens.

PN WO200192523-A2.

XX PD 06-DEC-2001.

XX PF 29-MAY-2001; 2001WO-US010836.

XX PR 30-MAY-2000; 2000US-0206132P.

XX PR 29-AUG-2000; 2000US-0228716P.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach MD;

XX DR WPI; 2002-106308/14.

XX DR P-PSDB; ABP08101.

XX PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.

XX PS Disclosure; SEQ ID NO 16183; 1037pp; English.

XX CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP0010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester

CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 321 BP; 105 A; 66 C; 74 G; 76 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 124 Length: 321
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABN23853 (1-321)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 249 GTATTGGTGGCGTTGGAAGATTCTGC 223
|||||

RESULT 30

AAC36788

ID AAC36788 standard; DNA; 503 BP.

XX AC AAC36788;

XX DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15080.

XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 30-APR-1999; 99US-0132407P.

XX PR 04-MAY-1999; 99US-0132484P.

XX PR 05-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 06-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.

PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 202 Length: 503
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x AAC36788 (1-503)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
|||
Db 74 GTGTTAGGAGGTTTGGTCAATTT 97

RESULT 31
ACA40032/c
ID ACA40032 standard; DNA; 537 BP.
XX
AC ACA40032;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #21689.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Mycoplasma pneumoniae.
XX
FN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU36162.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 27902; 1766pp; English.
XX

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 537 BP; 187 A; 115 C; 102 G; 133 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 217 Length: 537
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-40 (1-9) x ACA40032 (1-537)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||
Db 76 GTTGTAGCGGGCTGGTCAGTTTGC 50

RESULT 32
ADH61274
ID ADH61274 standard; DNA; 552 BP.
XX
AC ADH61274;
XX
DT 25-MAR-2004 (first entry)
XX
DE Soybean cytokinin oxidase (CKX1) DNA #3.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; soybean; ds; gene.
XX
OS Glycine max.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.
XX
PR 20-DEC-2001; 2001US-0343129P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX
DR WPI; 2003-897983/82.
DR GENBANK; BM528151.
XX
PT Producing plants characterized by reversible male-sterility, useful for

PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Disclosure; SEQ ID NO 15; 33pp; English.
XX
CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is soybean cytokinin oxidase (CKX1) DNA. This sequence is used
CC to illustrate the method of the invention.
XX
SQ Sequence 552 BP; 167 A; 106 C; 118 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 224 Length: 552
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADH61274 (1-552)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
Db 12 GTTCTTGAGGCTTAGGGCAATTT 35

RESULT 33
ADH61273
ID ADH61273 standard; DNA; 566 BP.
XX
AC ADH61273;
XX
DT 25-MAR-2004 (first entry)
XX
DE Soybean cytokinin oxidase (CKX1) DNA #2.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; soybean; ds; gene.
XX
OS Glycine max.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.
XX
PR 20-DEC-2001; 2001US-0343129P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX
DR WPI; 2003-897983/82.
DR GENBANK; BU084470.
XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Disclosure; SEQ ID NO 14; 33pp; English.
XX
CC The invention relates to a method for producing a plant characterised by

CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is soybean cytokinin oxidase (CKX1) DNA. This sequence is used
CC to illustrate the method of the invention.
XX
SQ Sequence 566 BP; 162 A; 115 C; 132 G; 157 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 230 Length: 566
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADH61273 (1-566)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
Db 283 GTTCTTGAGGCTTAGGGCAATTT 306

RESULT 34
ADH61277
ID ADH61277 standard; DNA; 582 BP.
XX
AC ADH61277;
XX
DT 25-MAR-2004 (first entry)
XX
DE Soybean cytokinin oxidase (CKX1) DNA #6.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; soybean; ds; gene.
XX
OS Glycine max.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.
XX
PR 20-DEC-2001; 2001US-0343129P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX
DR WPI; 2003-897983/82.
DR GENBANK; BM143498.
XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.
XX
PS Disclosure; SEQ ID NO 18; 33pp; English.
XX
CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing

CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is soybean cytokinin oxidase (CKX1) DNA. This sequence is used
CC to illustrate the method of the invention.

XX SQ Sequence 582 BP; 179 A; 112 C; 129 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 237 Length: 582
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADH61277 (1-582)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 58 GTTCTTGAGGCTTGGGACAAATT 81

RESULT 35
ADH61275
ID ADH61275 standard; DNA; 635 BP.
XX
AC ADH61275;
XX
DT 25-MAR-2004 (first entry)
XX
DE Soybean cytokinin oxidase. (CKX1) DNA #4.
XX
KW Male-sterility; cytokinin oxidase; transgenic plant; seed production;
KW CKX1; soybean; ds; gene.
XX
OS Glycine max.
XX
PN US2003163847-A1.
XX
PD 28-AUG-2003.
XX
PF 20-DEC-2002; 2002US-00326184.
XX
PR 20-DEC-2001; 2001US-0343129P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Huang S, Crossland LD, Cheikh N, Morris RO;
XX
DR WPI; 2003-897983/82.
DR GENBANK; BE330968.

XX
PT Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.

PS Disclosure; SEQ ID NO 16; 33pp; English.

XX
CC The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production
CC characteristics into plants having desirable characteristics. The present
CC sequence is soybean cytokinin oxidase (CKX1) DNA. This sequence is used
CC to illustrate the method of the invention.

XX SQ Sequence 635 BP; 198 A; 122 C; 137 G; 178 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 261 Length: 635
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x ADH61275 (1-635)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 108 GTTCTTGAGGCTTAGGGCAATT 131

RESULT 36
AAH34132
ID AAH34132 standard; cDNA; 1088 BP.
XX
AC AAH34132;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1214.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 15; ss.
XX
OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US026524.

XX PR 29-SEP-1999; 99US-0157137P.

XX PR 03-NOV-1999; 99US-0163280P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX DR WPI; 2001-235357/24.

XX DR P-PSDB; AAG74727.

XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.

XX PS Claim 1; Page 2995; 9803pp; English.

XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922

XX SQ Sequence 1088 BP; 309 A; 239 C; 261 G; 276 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.: 471 Length: 1088

Score: 41.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x AAH34132 (1-1088)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 59 CTCGGTGGCTGGGCTGTTCTGC 82.

RESULT 37

ABQ34200

ID ABQ34200 standard; DNA; 1234 BP.

XX AC ABQ34200;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20791.

XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX SQ Sequence 1234 BP; 205 A; 151 C; 498 G; 380 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 540 Length: 1234
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABQ34200 (1-1234)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 532 GTCTCGCGCGCTTGGTGAGTTTGC 558

RESULT 38

ABQ34201/C

ID ABQ34201 standard; DNA; 1234 BP.

XX AC ABQ34201;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20792.

XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

SQ Sequence 1234 BP; 380 A; 498 C; 151 G; 205 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 540 Length: 1234
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-40 (1-9) x ABQ34201 (1-1234)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 703 GTCGTCGGCGGCGTGGTGAGTTTGC 677

RESULT 39

AAS51508

ID AAS51508 standard; DNA; 1296 BP.

XX AAS51508;

DT 13-FEB-2002 (first entry)

DE Pseudomonas aeruginosa DNA for cellular proliferation protein #93.

KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.

OS Pseudomonas aeruginosa.

XX WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009180.

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

PA Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR P-PSDB; AAU33649.

XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.

PS Claim 27; SEQ ID NO 4090; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1296 BP; 172 A; 466 C; 384 G; 274 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 570 Length: 1296
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x AAS51508 (1-1296)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 1081 GTGATCGCGGCGCTCGGCGGCTTCTGC 1107

RESULT 40

ACA19484

ID ACA19484 standard; DNA; 1296 BP.

XX ACA19484;

DT 19-JUN-2003 (first entry)

DE Prokaryotic essential gene #1141.

KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.

OS Pseudomonas aeruginosa.

XX WO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR P-PSDB; ABU15614.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 14; SEQ ID NO 7354; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1296 BP; 172 A; 466 C; 384 G; 274 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 570 Length: 1296
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-40 (1-9) x ACA19484 (1-1296)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 1081 GTGATCGCGCGCCTCGGCGGCTTCTGC 1107

Search completed: February 18, 2005, 03:27:08
Job time : 190.74 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 02:33:38 ; Search time 53.1 Seconds
(without alignments)
277.335 Million cell updates/sec

Title: US-10-014-101B-40
Perfect score: 50
Sequence: 1 VLGLGQPC 9

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct. -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101 @CGN 1 1 124 @runat 16022005 075846 7970 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	43	86.0	5183	1 US-08-459-568-3	Sequence 3, Appli
C 2	43	86.0	5183	2 US-08-399-411-3	Sequence 3, Appli
C 3	43	86.0	5868	3 US-08-516-859A-3	Sequence 3, Appli
C 4	43	86.0	5868	3 US-09-586-472-3	Sequence 3, Appli
C 5	43	86.0	5868	3 US-09-528-706-3	Sequence 3, Appli
C 6	43	86.0	6173	4 US-09-949-016-5511	Sequence 5511, Ap
C 7	43	86.0	6173	4 US-09-949-016-5512	Sequence 5512, Ap
C 8	43	86.0	42672	4 US-09-949-016-17253	Sequence 17253, A
C 9	43	86.0	42672	4 US-09-949-016-17254	Sequence 17254, A
10	42	84.0	706	3 US-08-998-416-873	Sequence 873, App
C 11	41	82.0	1296	4 US-09-252-991A-3696	Sequence 3696, Ap
12	41	82.0	1368	4 US-09-252-991A-3813	Sequence 3813, Ap

13	41	82.0	1605	3 US-09-124-541-3	Sequence 3, Appli
14	41	82.0	1605	4 US-09-663-326-3	Sequence 3, Appli
15	41	82.0	2784	4 US-09-252-991A-3769	Sequence 3769, Ap
16	41	82.0	6733	3 US-09-124-541-2	Sequence 2, Appli
17	41	82.0	6733	4 US-09-663-326-2	Sequence 2, Appli
18	41	82.0	8473	3 US-09-172-422-2	Sequence 2, Appli
C 19	41	82.0	48763	4 US-09-916-204-3	Sequence 3, Appli
C 20	41	82.0	48763	4 US-10-282-048-3	Sequence 3, Appli
C 21	41	82.0	174493	4 US-09-804-471A-3	Sequence 3, Appli
C 22	41	82.0	174493	4 US-10-238-709-3	Sequence 3, Appli
C 23	40	80.0	601	4 US-09-949-016-73087	Sequence 73087, A
24	40	80.0	2611	4 US-09-620-312D-925	Sequence 925, App
C 25	40	80.0	168174	4 US-10-071-411A-63	Sequence 63, Appli
C 26	40	80.0	168273	4 US-10-071-411A-2	Sequence 2, Appli
27	40	80.0	194937	4 US-09-949-016-17032	Sequence 17032, A
28	40	80.0	194937	4 US-09-949-016-17033	Sequence 17033, A
29	40	80.0	221545	4 US-09-949-016-13875	Sequence 13875, A
30	40	80.0	784019	4 US-09-949-016-14033	Sequence 14033, A
31	40	80.0	828152	4 US-09-949-016-12777	Sequence 12777, A
32	39	78.0	283	2 US-08-691-814B-88	Sequence 88, Appli
33	39	78.0	284	2 US-08-691-814B-91	Sequence 91, Appli
34	39	78.0	303	2 US-08-691-814B-90	Sequence 90, Appli
35	39	78.0	325	2 US-08-691-814B-89	Sequence 89, Appli
C 36	39	78.0	2549	3 US-09-467-082-3	Sequence 3, Appli
C 37	39	78.0	2549	4 US-09-394-455-5	Sequence 5, Appli
C 38	39	78.0	2549	4 US-09-949-016-3584	Sequence 3584, Ap
C 39	39	78.0	2608	4 US-09-394-455-35	Sequence 35, Appli
40	39	78.0	3846	2 US-08-691-814B-3	Sequence 3, Appli
41	39	78.0	3846	4 US-09-949-016-821	Sequence 821, App
42	39	78.0	3860	4 US-09-949-016-3964	Sequence 3964, Ap
C 43	39	78.0	9053	4 US-09-976-594-306	Sequence 306, App
C 44	39	78.0	12425	4 US-09-616-289-50	Sequence 50, Appli
45	39	78.0	15353	4 US-09-949-016-13454	Sequence 13454, A

ALIGNMENTS

RESULT 1

US-08-459-568-3/c
; Sequence 3, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5183 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..5158
US-08-459-568-3

Alignment Scores:
Pred. No.: 154
Score: 43.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 86.00%
DB: 1
Length: 5183
Matches: 8
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0

US-10-014-101B-40 (1-9) x US-08-459-568-3 (1-5183)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1608 GTTCTGGTGGCCTGGCCCTGTTCTGC 1582

RESULT 2
US-08-399-411-3/c
; Sequence 3, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..5158
US-08-399-411-3

Alignment Scores:
Pred. No.: 154
Score: 43.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 86.00%

DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x US-08-399-411-3 (1-5183)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1608 GTTCTGGTGGCCTGGCCCTGTTCTGC 1582

RESULT 3
US-08-516-859A-3/c
; Sequence 3, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..5278
US-08-516-859A-3

Alignment Scores:
Pred. No.: 178
Score: 43.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 86.00%
DB: 3
Length: 5868
Matches: 8
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0

US-10-014-101B-40 (1-9) x US-08-516-859A-3 (1-5868)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1728 GTTCTGGTGGCCTGGCCCTGTTCTGC 1702

RESULT 4
US-09-586-472-3/c

; Sequence 3, Application US/09586472
; Patent No. 632335
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/586,472
; FILING DATE: 01-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..5278
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-586-472-3
Alignment Scores:
Pred. No.: 178 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 3 Gaps: 0
US-10-014-101B-40 (1-9) x US-09-586-472-3 (1-5868)
Qy 1 ValLeuGlyLeuGlyGlnPheCys 9
Db 1728 GTTCTGGTGGCTGGCCCTGTTCTGC 1702
RESULT 5
US-09-528-706-3/c
; Sequence 3, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; Zinc Finger Proteins

; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..5278
; INFORMATION FOR SEQ ID NO: 3:
US-09-528-706-3
Alignment Scores:
Pred. No.: 178 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 3 Gaps: 0
US-10-014-101B-40 (1-9) x US-09-528-706-3 (1-5868)
Qy 1 ValLeuGlyLeuGlyGlnPheCys 9
Db 1728 GTTCTGGTGGCTGGCCCTGTTCTGC 1702
RESULT 6
US-09-949-016-5511/c
; Sequence 5511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5511
; LENGTH: 6173
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5511

Alignment Scores:
Pred. No.: 190 Length: 6173
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-5511 (1-6173)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 1182 GTTCTGGGTGGCCTGGGCCTGTTCTGC 1156

RESULT 7

US-09-949-016-5512/c
; Sequence 5512, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5512
; LENGTH: 6173
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5512

Alignment Scores:

Pred. No.: 190 Length: 6173
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-5512 (1-6173)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 1182 GTTCTGGGTGGCCTGGGCCTGTTCTGC 1156

RESULT 8

US-09-949-016-17253/c
; Sequence 17253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17253
; LENGTH: 42672
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17253

Alignment Scores:
Pred. No.: 1.89e+03 Length: 42672
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-17253 (1-42672)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 31998 GTTCTGGGTGGCCTGGGCCTGTTCTGC 31972

RESULT 9

US-09-949-016-17254/c
; Sequence 17254, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17254
; LENGTH: 42672
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17254

Alignment Scores:

Pred. No.: 1.89e+03 Length: 42672
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-17254 (1-42672)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 31998 GTTCTGGGTGGCCTGGGCCTGTTCTGC 31972

RESULT 10

US-08-998-416-873
; Sequence 873, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:

; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine

APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebeschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 873:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1548RP
ORGANISM: Pseudomonas aeruginosa
US-08-998-416-873

Alignment Scores:
Pred. No.: 22.8 Length: 706
Score: 42.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x US-08-998-416-873 (1-706)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 344 CTGGCGGGTTGGCAGTTCTGTC 367

RESULT 11

US-09-252-991A-3696/c
Sequence 3696, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3696
LENGTH: 1296
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3696
Alignment Scores:
Pred. No.: 74.3 Length: 1296
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-252-991A-3696 (1-1296)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 225 GTGATCGGGCGCCTCGGGCGGCTTCTGC 199

RESULT 12

US-09-252-991A-3813
Sequence 3813, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3813
LENGTH: 1368
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3813

Alignment Scores:

Pred. No.: 79.3 Length: 1368
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-252-991A-3813 (1-1368)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1153 GTGATCGGGCGCCTCGGGCGGCTTCTGC 1179

RESULT 13

US-09-124-541-3
Sequence 3, Application US/09124541A
Patent No. 6229066
GENERAL INFORMATION:
APPLICANT: Morris Ph.D., Roy O.
TITLE OF INVENTION: A CYTOKININ OXIDASE
FILE REFERENCE: UMO1490
CURRENT APPLICATION NUMBER: US/09/124,541A
CURRENT FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: 60/054,268
EARLIER FILING DATE: 1997-07-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1605

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-124-541-3

Alignment Scores:
Pred. No.: 95.9 Length: 1605
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-124-541-3 (1-1605)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
|||||
Db 673 GTCCTGGCGGGCTGGGGCAGTTC 696

RESULT 14

US-09-663-326-3

; Sequence 3, Application US/09663326
; Patent No. 6617497

; GENERAL INFORMATION:

; APPLICANT: Morris Ph.D., Roy O.

; TITLE OF INVENTION: A CYTOKININ OXIDASE

; FILE REFERENCE: UMO1490

; CURRENT APPLICATION NUMBER: US/09/663,326

; CURRENT FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: 60/054,268

; PRIOR FILING DATE: 1997-07-30

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1605

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1605)

US-09-663-326-3

Alignment Scores:

Pred. No.: 95.9 Length: 1605
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-663-326-3 (1-1605)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
|||||
Db 673 GTCCTGGCGGGCTGGGGCAGTTC 696

RESULT 15

US-09-252-991A-3769

; Sequence 3769, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3769
; LENGTH: 2784
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3769

Alignment Scores:
Pred. No.: 184 Length: 2784
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-252-991A-3769 (1-2784)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 1118 GTGATCGCGGCCTCGGGCTTCTGC 1144

RESULT 16

US-09-124-541-2

; Sequence 2, Application US/09124541A

; Patent No. 6229066

; GENERAL INFORMATION:

; APPLICANT: Morris Ph.D., Roy O.

; TITLE OF INVENTION: A CYTOKININ OXIDASE

; FILE REFERENCE: UMO1490

; CURRENT APPLICATION NUMBER: US/09/124,541A

; CURRENT FILING DATE: 1998-07-29

; EARLIER APPLICATION NUMBER: 60/054,268

; EARLIER FILING DATE: 1997-07-30

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 6733

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: gene

; LOCATION: (1)..(6733)

; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea

; OTHER INFORMATION: mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1497)..(2111)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2524)..(3216)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3311)..(3607)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (5697)

US-09-124-541-2

Alignment Scores:

Pred. No.: 527 Length: 6733
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-124-541-2 (1-6733)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
|||||
Db 2581 GTCCTGGCGGGCTGGGGCAGTTC 2604

RESULT 17

US-09-663-326-2
; Sequence 2, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-663-326-2

Alignment Scores:
Pred. No.: 527 Length: 6733
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-663-326-2 (1-6733)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
|||||
Db 2581 GTCTGGGCGGCTGGGGCAGTTC 2604

RESULT 18
US-09-172-422-2
; Sequence 2, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet
; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/172,422A
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-172-422-2
Alignment Scores:

Pred. No.: 692 Length: 8473
Score: 41.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-172-422-2 (1-8473)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 59 CTCGGTGGCCTCGGCTCGTTCTGC 82

RESULT 19

US-09-916-204-3/c

; Sequence 3, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 48763
; TYPE: DNA
; ORGANISM: Human
US-09-916-204-3

Alignment Scores:
Pred. No.: 5.54e+03 Length: 48763
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-916-204-3 (1-48763)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 23030 GTTCTGGGGAATGGGGAGGTATTGT 23004

RESULT 20

US-10-282-048-3/c

; Sequence 3, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 48763
; TYPE: DNA
; ORGANISM: Human
US-10-282-048-3

Alignment Scores:
Pred. No.: 5.54e+03 Length: 48763
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 82.00% Indels: 0

; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 925
; LENGTH: 2611
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (290)..(1885)
US-09-620-312D-925

Alignment Scores:
Pred. No.: 271 Length: 2611
Score: 40.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-620-312D-925 (1-2611)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 101 GTCCTCGGGCGCTGGTGGCTACTGC 127
:::

RESULT 25

US-10-071-411A-63/c
; Sequence 63, Application US/10071411A
; Patent No. 6797475
; GENERAL INFORMATION:
; APPLICANT: Glenn Barnes
; APPLICANT: Joanne Meyer
; TITLE OF INVENTION: Detection of Polymorphisms in the Human
; TITLE OF INVENTION: 5-Lipoxygenase Gene
; FILE REFERENCE: MRI-021
; CURRENT APPLICATION NUMBER: US/10/071,411A
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/267,515
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/314,248
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 168174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(168174)
; OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-63

Alignment Scores:
Pred. No.: 3.79e+04 Length: 168174
Score: 40.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-071-411A-63 (1-168174)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||

Db 22730 GTTCTGGCAGGGCTGGGGAGATTCTGC 22704

RESULT 26

US-10-071-411A-2/c
; Sequence 2, Application US/10071411A
; Patent No. 6797475
; GENERAL INFORMATION:
; APPLICANT: Glenn Barnes
; APPLICANT: Joanne Meyer
; TITLE OF INVENTION: Detection of Polymorphisms in the Human
; TITLE OF INVENTION: 5-Lipoxygenase Gene
; FILE REFERENCE: MRI-021
; CURRENT APPLICATION NUMBER: US/10/071,411A
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/267,515
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/314,248
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(168273)
; OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-2

Alignment Scores:
Pred. No.: 3.79e+04 Length: 168273
Score: 40.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-071-411A-2 (1-168273)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 22780 GTTCTGGCAGGGCTGGGGAGATTCTGC 22754
:::

RESULT 27

US-09-949-016-17032
; Sequence 17032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17032
; LENGTH: 194937
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17032

Alignment Scores:
Pred. No.: 4.51e+04 Length: 194937
Score: 40.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1

Best Local Similarity: 77.78% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-17032 (1-194937)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 28384 GTGCTAGGAGGAAGTGGGAGGTTTGT 28410

RESULT 28

US-09-949-016-17033
; Sequence 17033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17033
; LENGTH: 194937
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17033

Alignment Scores:

Pred. No.: 4.51e+04 Length: 194937
Score: 40.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-17033 (1-194937)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 28384 GTGCTAGGAGGAAGTGGGAGGTTTGT 28410

RESULT 29

US-09-949-016-13875
; Sequence 13875, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13875
; LENGTH: 221545
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13875

Alignment Scores:

Pred. No.: 5.24e+04 Length: 221545
Score: 40.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-13875 (1-221545)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 198801 GTGGCAGGAGGTTTGGGTTCTCTTCTGC 198827

RESULT 30

US-09-949-016-14033
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14033
; LENGTH: 784019
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(784019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033

Alignment Scores:

Pred. No.: 2.27e+05 Length: 784019
Score: 40.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-14033 (1-784019).

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 254504 CTGGGAGGACTGGACAGATCTGT 254527

RESULT 31

US-09-949-016-12777
; Sequence 12777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 12777
;; LENGTH: 828152
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(828152)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Alignment Scores:
Pred. No.: 2.41e+05 Length: 828152
Score: 40.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 80.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-12777 (1-828152)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 250637 CTGGGAGGACTGGGACAGATCTGT 250660

RESULT 32

US-08-691-814B-88
; Sequence 88, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA

US-08-691-814B-88

Alignment Scores:
Pred. No.: 30.5 Length: 283
Score: 39.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 78.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x US-08-691-814B-88 (1-283)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 38 GTCTGGGTGGCGCTGGTGCATCTGT 64

RESULT 33

US-08-691-814B-91
; Sequence 91, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA

Alignment Scores:
Pred. No.: 30.7 Length: 284
Score: 39.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 78.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x US-08-691-814B-91 (1-284)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 211 GTCTTGGTGGCGCTGGTGCAATTCGT 237

RESULT 34
US-08-691-814B-90
; Sequence 90, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-691-814B-90

Alignment Scores:
Pred. No.: 33.1 Length: 303
Score: 39.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 78.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x US-08-691-814B-90 (1-303)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 132 GTCTTGGTGGCGCTGGTGCAATTCGT 158

RESULT 35
US-08-691-814B-89
; Sequence 89, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul

; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-691-814B-89

Alignment Scores:
Pred. No.: 36 Length: 325
Score: 39.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 78.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x US-08-691-814B-89 (1-325)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 1 GTCTTGGTGGCGCTGGTGCAATTCGT 27

RESULT 36
US-09-467-082-3/c
; Sequence 3, Application US/09467082
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0088
; CURRENT APPLICATION NUMBER: US/09/467,082
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)..(1136)
; NAME/KEY: unsure
; LOCATION: 6

; OTHER INFORMATION: unknown
US-09-467-082-3

Alignment Scores:
Pred. No.: 416 Length: 2549
Score: 39.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 78.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-467-082-3 (1-2549)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 2169 TTGGGGGACTTGGCCTCTTCTGT 2146

RESULT 37

US-09-394-455-5/c

; Sequence 5, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustín, Jovenal
; APPLICANT: Leszyk, John D.
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: 07917/078001
; CURRENT APPLICATION NUMBER: US/09/394,455
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099,771
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

; LENGTH: 2549

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (81)...(1133)

; NAME/KEY: misc feature

; LOCATION: (1)...(2549)

; OTHER INFORMATION: n = A,T,C or G

US-09-394-455-5

Alignment Scores:

Pred. No.: 416 Length: 2549
Score: 39.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 78.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-394-455-5 (1-2549)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 2169 TTGGGGGACTTGGCCTCTTCTGT 2146

RESULT 38

US-09-949-016-3584/c

; Sequence 3584, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3584
; LENGTH: 2549
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3584

Alignment Scores:

Pred. No.: 416 Length: 2549
Score: 39.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 78.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-949-016-3584 (1-2549)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 2168 TTGGGGGACTTGGCCTCTTCTGT 2145

RESULT 39

US-09-394-455-35/c

; Sequence 35, Application US/09394455
; Patent No. 6531305

; GENERAL INFORMATION:

; APPLICANT: Witman, George F.

; APPLICANT: San Agustín, Jovenal

; APPLICANT: Leszyk, John D.

; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING

; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE

; FILE REFERENCE: 07917/078001

; CURRENT APPLICATION NUMBER: US/09/394,455

; CURRENT FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: US 60/099,771

; PRIOR FILING DATE: 1998-09-10

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 2608

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (164)...(1192)

US-09-394-455-35

Alignment Scores:

Pred. No.: 428 Length: 2608
Score: 39.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 78.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-394-455-35 (1-2608)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 2228 TTGGGGGACTTGGCCTCTTCTGT 2205

RESULT 40

US-08-691-814B-3

; Sequence 3, Application US/08691814B

; Patent No. 5981218

; GENERAL INFORMATION:

; APPLICANT: Rio, Marie-Christine

; APPLICANT: Tomasetto, Catherine

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 05:26:14 ; Search time 424.26 Seconds
(without alignments)
125.382 Million cell updates/sec

Title: US-10-014-101B-40
Perfect score: 50
Sequence: 1 VLGGGQFC 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US10014101/runat_16022005_075848_8061/app_query.fasta_1.796
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10014101@cgn 1 1 659 @runat_16022005_075848_8061
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUB.seq:
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	45	90.0	65047	13	US-10-087-192-259	Sequence 259, Appl
2	43	86.0	503	16	US-10-029-386-9173	Sequence 9173, Ap
3	43	86.0	789	16	US-10-029-386-22854	Sequence 22854, A
c 4	43	86.0	5868	14	US-10-024-450-3	Sequence 3, Appli
5	43	86.0	6113	15	US-10-311-455-1795	Sequence 1795, Ap
6	43	86.0	6436	15	US-10-311-455-654	Sequence 654, App
7	43	86.0	7603	15	US-10-311-455-281	Sequence 281, App
8	43	86.0	7603	16	US-10-240-452-29	Sequence 29, Appl
9	43	86.0	9504	15	US-10-240-453-281	Sequence 281, App
10	43	86.0	254087	13	US-10-087-192-223	Sequence 223, App
11	42	84.0	556	18	US-10-425-115-102522	Sequence 102522,
c 12	42	84.0	564	13	US-10-027-632-280541	Sequence 280541,
c 13	42	84.0	564	17	US-10-027-632-280541	Sequence 280541,
c 14	42	84.0	1230	17	US-10-424-599-70249	Sequence 70249, A
c 15	42	84.0	2139	18	US-10-437-963-82245	Sequence 82245, A
16	42	84.0	7329	17	US-10-221-714A-396	Sequence 396, App
17	42	84.0	13321	17	US-10-221-714A-143	Sequence 143, App
18	42	84.0	3673778	16	US-10-312-841-1	Sequence 1, Appli
19	41	82.0	201	18	US-10-741-601-10567	Sequence 10567, A
20	41	82.0	201	19	US-10-741-600-26062	Sequence 26062, A
c 21	41	82.0	255	10	US-09-930-213-609	Sequence 609, App
22	41	82.0	369	18	US-10-425-115-74928	Sequence 74928, A
c 23	41	82.0	537	17	US-10-282-122A-27902	Sequence 27902, A
24	41	82.0	552	16	US-10-326-184-15	Sequence 15, Appl
25	41	82.0	566	16	US-10-326-184-14	Sequence 14, Appl
26	41	82.0	582	16	US-10-326-184-18	Sequence 18, Appl
27	41	82.0	588	18	US-10-425-115-94827	Sequence 94827, A
28	41	82.0	635	16	US-10-326-184-16	Sequence 16, Appl
29	41	82.0	1088	15	US-10-106-698-1224	Sequence 1224, Ap
30	41	82.0	1141	17	US-10-425-114-10886	Sequence 10886, A
31	41	82.0	1142	17	US-10-424-599-1725	Sequence 1725, Ap
32	41	82.0	1234	18	US-10-363-345A-20791	Sequence 20791, A
c 33	41	82.0	1234	18	US-10-363-345A-20792	Sequence 20792, A
34	41	82.0	1238	18	US-10-437-963-81681	Sequence 81681, A
35	41	82.0	1257	17	US-10-425-114-3248	Sequence 3248, Ap
36	41	82.0	1258	18	US-10-425-115-150790	Sequence 150790,
37	41	82.0	1279	17	US-10-425-114-8021	Sequence 8021, Ap
38	41	82.0	1296	9	US-09-815-242-4090	Sequence 4090, Ap
39	41	82.0	1296	17	US-10-282-122A-7354	Sequence 7354, Ap
40	41	82.0	1318	17	US-10-424-599-9802	Sequence 9802, Ap
41	41	82.0	1318	17	US-10-424-599-12845	Sequence 12845, A
42	41	82.0	1506	14	US-10-014-101-26	Sequence 26, Appl
43	41	82.0	1506	16	US-10-326-184-8	Sequence 8, Appli
44	41	82.0	1506	17	US-10-311-453-26	Sequence 26, Appl
45	41	82.0	1515	14	US-10-014-101-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-087-192-259
; Sequence 259, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 65047

; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(65047)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-259

Alignment Scores:
Pred. No.: 2.31e+03 Length: 65047
Score: 45.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 90.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-087-192-259 (1-65047)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 36758 GTTCTGGAGGTTGGGGTCCTTTTGT 36784

RESULT 2

US-10-029-386-9173
; Sequence 9173, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9173
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031277.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: gi7705546, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q01101, EVALUE 3.00e-05
; OTHER INFORMATION: EST_HUMAN HIT: AI808800.1, EVALUE 1.00e-82
US-10-029-386-9173

Alignment Scores:
Pred. No.: 44.3 Length: 503
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-029-386-9173 (1-503)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 4 GTTCTGGGTGGCCTGGGCCTGTTCTGC 30

RESULT 3

US-10-029-386-22854.
; Sequence 22854, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22854
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031277.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
; OTHER INFORMATION: SWISSPROT HIT: P57071, EVALUE 3.20e-01
; OTHER INFORMATION: NT HIT: gi16168391, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BG942814.1, EVALUE 0.00e+00
US-10-029-386-22854

Alignment Scores:
Pred. No.: 69.4 Length: 789
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-029-386-22854 (1-789)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 468 GTTCTGGGTGGCCTGGGCCTGTTCTGC 494

RESULT 4

US-10-024-450-3/c
; Sequence 3, Application US/10024450
; Publication No. US20030032606A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; APPLICANT: Chadwick, Robert B.
; TITLE OF INVENTION: Methods of Detecting and Treating
; TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
; FILE REFERENCE: P-LJ 5101
; CURRENT APPLICATION NUMBER: US/10/024,450
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,582
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5868
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)...(5277)
US-10-024-450-3

Alignment Scores:
Pred. No.: 511 Length: 5868
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-024-450-3 (1-5868)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 1728 GTTCTGGGTGGCCTGGGCCTGTTCTGC 1702

RESULT 5

US-10-311-455-1795
; Sequence 1795, Application US/10311455
; Publication No. US20030143606A1

```

; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1795
; LENGTH: 6113

```

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1795

Alignment Scores:		
Pred. No.:	533	6113
Score:	43.00	
Percent Similarity:	88.89%	Length:
Best Local Similarity:	88.89%	Matches:
Query Match:	86.00%	Conservative:
DB:	15	Mismatches:
		Indels:
		Gaps:

US-10-014-101B-40 (1-9) x US-10-311-455-1795 (1-6113)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||
Db 5780 GTTTCGGTGGGTACGTGTTTGT 5

RESULT 6

US-10-311-455-654
; Sequence 654, Application US/10311455
; Publication No. US20030143606A1

```

; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 654
; LENGTH: 6436

```

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-654

Alignment Scores: 561
Pred. No.: 561
Length: 6436

Score:	43.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	86.00%	Indels:	0
DB:	15	Gaps:	0

US-10-014-101B-40 (1-9) x US-10-311-455-654 (1-6436)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||
5764 GTTTTGGSTGGGTAGGTGTTTTTGC 5790
pb

RESULT 7

US-10-311-455-281
; Sequence 281, Application US/10311455
; Publication No. US20030143606A1

```

; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 281
; LENGTH: 7603
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-281

Alignment Scores:		
Pred. No.:	662	7603
Score:	43.00	Length:
Percent Similarity:	88.89%	Matches:
Best Local Similarity:	88.89%	Conservative:
Query Match:	86.00%	Mismatches:
DB:	15	Indels:
		Gaps:

US-10-014-101B-40 (1-9) x US-10-311-455-281 (1-7603)

Qy	1	V	a	l	l	e	u	G	l	y	G	l	y	L	e	u	G	l	y	G	l	n	P	h	e	C	y	s	9
Dβ	334	G	T	T	T	G	G	T	T	A	C	G	T	T	T	T	T	T	G	T	3								

RESULT 8

US-10-240-452-29
; Sequence 29, Application US/10240452
; Publication No. US20030162194A1

; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with Apoptosis
 ; FILE REFERENCE: 5013.1006
 ; CURRENT APPLICATION NUMBER: US/10/240,452
 ; CURRENT FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03969
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019058.8
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 29
; LENGTH: 7603
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-452-29

Alignment Scores:
Pred. No.: 662 Length: 7603
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-240-452-29 (1-7603)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 334 GTTTGGGTGGGTAGGTGTTTTTGT 360

RESULT 9

US-10-240-453-281
; Sequence 281, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; TITLE OF INVENTION: With DNA Transcription
; FILE REFERENCE: 5013.1009

CURRENT APPLICATION NUMBER: US/10/240.453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350

SEQ ID NO 281
LENGTH: 9504

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-281

Alignment Scores:
Pred. No.: 826 Length: 9504
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 15 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-240-453-281 (1-9504)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 6626 GTTTGGGTGGGTAGGTGTTTTTGT 6652

RESULT 10
US-10-087-192-223
; Sequence 223, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 254087

TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(254087)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-223

Alignment Scores:

Pred. No.: 2.18e+04 Length: 254087
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-087-192-223 (1-254087)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 241873 GTACTGGAGGCTTGGTTGTTTTC 241899

RESULT 11

US-10-425-115-102522
; Sequence 102522, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With.
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 102522
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_25007C.1
US-10-425-115-102522

Alignment Scores:
Pred. No.: 76.3 Length: 556
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-115-102522 (1-556)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 510 TTGGGGGGCTGGGGCGGTTTGT 533

RESULT 12

US-10-027-632-280541/c
; Sequence 280541, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME

; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280541
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-280541

Alignment Scores:
Pred. No.: 77.4 Length: 564
Score: 42.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-027-632-280541 (1-564)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 110 GTGCTGGGACCCCTGGGCCAGTTCTGT 84

RESULT 13

US-10-027-632-280541/c
; Sequence 280541, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME

; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280541
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-280541

Alignment Scores:
Pred. No.: 77.4 Length: 564
Score: 42.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-027-632-280541 (1-564)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 110 GTGCTGGGACCCCTGGGCCAGTTCTGT 84

RESULT 14

US-10-424-599-70249/c
; Sequence 70249, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 70249
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Glycine max

US-10-424-599-70249

Alignment Scores:
Pred. No.: 168 Length: 1230
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-424-599-70249 (1-1230)

Qy 3 GlyGlyLeuGlyGlnPheCys 9
|||||
Db 220 GGAGGGTTGGGCCAGTTCTGC 200

RESULT 15

US-10-437-963-82245/c
; Sequence 82245, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

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; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82245
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81694C.1
US-10-437-963-82245

Alignment Scores:
Pred. No.: 292 Length: 2139
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-437-963-82245 (1-2139)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 2137 ATCGTAGGAGGTCTCGGAAGGTTTGT 2111

RESULT 16
US-10-221-714A-396
; Sequence 396, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 396
; LENGTH: 7329
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

Alignment Scores:
Pred. No.: 994 Length: 7329
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-437-963-82245 (1-2139)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 2137 ATCGTAGGAGGTCTCGGAAGGTTTGT 2111

RESULT 17
US-10-221-714A-143
; Sequence 143, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 143
; LENGTH: 13321
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

Alignment Scores:
Pred. No.: 13321 Length: 13321
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-221-714A-143 (1-13321)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 10259 GTTATAGGTTGTCGGAAGATTTTGT 10285

RESULT 18
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
```

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; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82245
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81694C.1
US-10-437-963-82245

Alignment Scores:
Pred. No.: 292 Length: 2139
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-437-963-82245 (1-2139)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 2137 ATCGTAGGAGGTCTCGGAAGGTTTGT 2111

RESULT 16
US-10-221-714A-396
; Sequence 396, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 396
; LENGTH: 7329
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

Alignment Scores:
Pred. No.: 994 Length: 7329
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-437-963-82245 (1-2139)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 2137 ATCGTAGGAGGTCTCGGAAGGTTTGT 2111

RESULT 17
US-10-221-714A-143
; Sequence 143, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 143
; LENGTH: 13321
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

Alignment Scores:
Pred. No.: 13321 Length: 13321
Score: 42.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-221-714A-143 (1-13321)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 10259 GTTATAGGTTGTCGGAAGATTTTGT 10285

RESULT 18
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
```

;
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Alignment Scores:
Pred. No.: 4.74e+05 Length: 3673778
Score: 42.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-312-841-1 (1-3673778)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 223774 ATTTGGCGGGTAGGTGTTTTTGT 223800

RESULT 19

US-10-741-601-10567

; Sequence 10567, Application US/10741601
; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 10567

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-741-601-10567

Alignment Scores:

Pred. No.: 43.2 Length: 201
Score: 41.00 Matches: 6
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-741-601-10567 (1-201)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 6 GTTATGGAGGCATTGGAAGTTTTCG 32

RESULT 20

US-10-741-600-26062

; Sequence 26062, Application US/10741600
; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 26062

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-741-600-26062

Alignment Scores:

Pred. No.: 43.2 Length: 201
Score: 41.00 Matches: 6
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 19 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-741-600-26062 (1-201)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 6 GTTATGGAGGCATTGGAAGTTTTCG 32

RESULT 21

US-09-930-213-609/c

; Sequence 609, Application US/09930213

; Publication No. US20030170625A1

; GENERAL INFORMATION:

; APPLICANT: ROSENTHAL, ANDRE

; APPLICANT: HINZMANN, BERND

; APPLICANT: SCHAFER, REINHARD

; APPLICANT: ZUBER, JOHANNES

; APPLICANT: TCHE-NITSE, OLEG

; APPLICANT: GRIPS, MARTIN

; APPLICANT: HELLNEGEL, MARTIN

; APPLICANT: SCHMITZ, ANNE-CHANTAL

; APPLICANT: SERS, CHRISTINE

; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS

; FILE REFERENCE: ALBRE-14

; CURRENT APPLICATION NUMBER: US/09/930,213

; CURRENT FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: DE 10004102.7

; PRIOR FILING DATE: 2000-01-31

; NUMBER OF SEQ ID NOS: 885

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 609

; LENGTH: 255

; TYPE: DNA

; ORGANISM: Rattus sp.

US-09-930-213-609

Alignment Scores:

Pred. No.: 54.7 Length: 255
Score: 41.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-930-213-609 (1-255)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9

Db 179 CTGGGTGGTGGCCATTTCGT 156

RESULT 22

US-10-425-115-74928

; Sequence 74928, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: KOVALIC, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326


```
; SEQ ID NO 74928
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_168330C.1
US-10-425-115-74928

Alignment Scores:
Pred. No.: 79 Length: 369
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-115-74928 (1-369)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 77 GTGCTGGAGGCGCTGGGGCAGTTC 100

RESULT 23
US-10-282-122A-27902/c
; Sequence 27902, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27902
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Mycoplasma pneumoniae
US-10-282-122A-27902

Alignment Scores:
Pred. No.: 121 Length: 566
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
```

```
Pred. No.: 115 Length: 537
Score: 41.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-282-122A-27902 (1-537)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
| | | | | | | | | | | | | | | | | |
Db 76 GTTGTAAAGCGGCTTGGTCAGTTTGC 50

RESULT 24
US-10-326-184-15
; Sequence 15, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Glycine max
US-10-326-184-15

Alignment Scores:
Pred. No.: 118 Length: 552
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-326-184-15 (1-552)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 12 GTTCTGGAGGCTTAGGGCAATTT 35

RESULT 25
US-10-326-184-14
; Sequence 14, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Glycine max
US-10-326-184-14

Alignment Scores:
Pred. No.: 121 Length: 566
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-326-184-14 (1-566)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 283 GTTCTTGAGGCTTAGGGCAATTT 306

RESULT 26

US-10-326-184-18
; Sequence 18, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Glycine max
US-10-326-184-18

Alignment Scores:
Pred. No.: 124 Length: 582
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-326-184-18 (1-582)

Qy 1 valLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 58 GTTCTTGAGGCTTAGGGCAATTT 81

RESULT 27

US-10-425-115-94827
; Sequence 94827, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 94827
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_186474C.1
US-10-425-115-94827

Alignment Scores:
Pred. No.: 126 Length: 588
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 82.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-115-94827 (1-588)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 71 GTCCTGGCGGGCTGGGCCAGTTC 94

RESULT 28

US-10-326-184-16
; Sequence 16, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Glycine max
US-10-326-184-16

Alignment Scores:
Pred. No.: 136 Length: 635
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 16 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-326-184-16 (1-635)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
| | | | | | | | | | | | | | | | | |
Db 108 GTTCTTGAGGCTTAGGGCAATTT 131

RESULT 29

US-10-106-698-1224
; Sequence 1224, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1224
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (158)..(158)
; OTHER INFORMATION: n equals a,t,g, or c

```
US-10-106-698-1224
Alignment Scores:
Pred. No.: 232
Score: 41.00
Percent Similarity: 87.50%
Best Local Similarity: 87.50%
Query Match: 82.00%
DB: 15
Length: 1088
Matches: 7
Conservative: 0
Mismatch: 1
Indels: 0
Gaps: 0

US-10-014-101B-40 (1-9) x US-10-106-698-1224 (1-1088)
QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
Db 59 CTCGGTGGCCTCGGCTCGTTCTGC 82

RESULT 30
US-10-425-114-10886
; Sequence 10886, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10886
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700985454_FLI
US-10-425-114-10886
Alignment Scores:
Pred. No.: 243
Score: 41.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 82.00%
DB: 17
Length: 1141
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-114-10886 (1-1141)
QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
Db 58 GTTCTAGGGGGGCTTGGCCAATT 81

RESULT 31
US-10-424-599-1725
; Sequence 1725, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1725
; LENGTH: 1142
; TYPE: DNA
```

```
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101557C.1
US-10-424-599-1725
Alignment Scores:
Pred. No.: 243
Score: 41.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 82.00%
DB: 17
Length: 1142
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-014-101B-40 (1-9) x US-10-424-599-1725 (1-1142)
QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8
Db 59 GTTCTAGGGGGGCTTGGCCAATT 82

RESULT 32
US-10-363-345A-20791
; Sequence 20791, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20791
; LENGTH: 1234
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-20791
Alignment Scores:
Pred. No.: 263
Score: 41.00
Percent Similarity: 100.00%
Best Local Similarity: 66.67%
Query Match: 82.00%
DB: 18
Length: 1234
Matches: 6
Conservative: 3
Mismatch: 0
Indels: 0
Gaps: 0

US-10-014-101B-40 (1-9) x US-10-363-345A-20791 (1-1234)
QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 532 GTCGTCGGGGGCTTGGTGAGTTTGC 558

RESULT 33
US-10-363-345A-20792/c
; Sequence 20792, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20792
; LENGTH: 1234
; TYPE: DNA
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20792
US-10-363-345A-20792

Alignment Scores:
Pred. No.: 263 Length: 1234
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-363-345A-20792 (1-1234)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 703 GTCGTCCGCGCGTGTGGTGGTTTTC 677

RESULT 34

US-10-437-963-81681

; Sequence 81681, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 81681

; LENGTH: 1238

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_81183C.1

US-10-437-963-81681

Alignment Scores:
Pred. No.: 264 Length: 1238
Score: 41.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-437-963-81681 (1-1238)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 180 GTTTTGGGGTCTTGGCAGTTCTGC 206

RESULT 35

US-10-425-114-3248

; Sequence 3248, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3248
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700244432_FLI
US-10-425-114-3248

Alignment Scores:
Pred. No.: 268 Length: 1257
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-114-3248 (1-1257)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8

Db 87 GTGCTGGCGGGCTGGGCCAGTTC 110

RESULT 36

US-10-425-115-150790

; Sequence 150790, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 150790

; LENGTH: 1258

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_69041C.1

US-10-425-115-150790

Alignment Scores:
Pred. No.: 268 Length: 1258
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-115-150790 (1-1258)

QY 1 ValLeuGlyGlyLeuGlyGlnPhe 8

Db 87 GTGCTGGCGGGCTGGGCCAGTTC 110

RESULT 37

US-10-425-114-8021

; Sequence 8021, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8021
LENGTH: 1279
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700731265_FLI
US-10-425-114-8021

Alignment Scores:
Pred. No.: 272 Length: 1279
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-425-114-8021 (1-1279)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8
Db 21 GTACTTGGAGGCTAGGTCAAGTTT 44

RESULT 38
US-09-815-242-4090
Sequence 4090, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4090
LENGTH: 1296
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-4090

Alignment Scores:
Pred. No.: 276 Length: 1296
Score: 41.00 Matches: 7

Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-40 (1-9) x US-09-815-242-4090 (1-1296)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db .1081 GTGATCGGGCGCCTCGGGCGCTTCTGC 1107

RESULT 39

US-10-282-122A-7354
Sequence 7354, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7354
LENGTH: 1296
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-7354

Alignment Scores:
Pred. No.: 276 Length: 1296
Score: 41.00 Matches: 7

Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 82.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-40 (1-9) x US-10-282-122A-7354 (1-1296)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db .1081 GTGATCGGGCGCCTCGGGCGCTTCTGC 1107

Db 1081 GTGATCGGGCGCTCGGGCTTCTGC 1107

RESULT 40

US-10-424-599-9802

; Sequence 9802, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 9802

; LENGTH: 1318

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_108862C.1

US-10-424-599-9802

Alignment Scores:

Pred. No.:	281	Length:	1318
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	82.00%	Indels:	0
DB:	17	Gaps:	0

US-10-014-101B-40 (1-9) x US-10-424-599-9802 (1-1318)

Qy 1 ValLeuGlyGlyLeuGlyGlnPhe 8

Db 778 GTTCTTGAGGCTTAGGGCAATTT 801

Search completed: February 18, 2005, 10:15:49

Job time : 633.26 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 02:20:24 ; Search time 1061.28 Seconds
(without alignments)
322.797 Million cell updates/sec

Title: US-10-014-101B-40
Perfect score: 50
Sequence: 1 VLGLGQFC 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10014101/runat 16022005 075846 7952/app query.fasta 1.796
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101 @CGN 1 1 5453 @runat 16022005 075846 7952 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	911	8	BZ178637 CH230-456
C 2	47	94.0	562	7	CK375056 lai44c10.
C 3	46	92.0	415	9	CL895276 abg31h01.
4	46	92.0	951	5	BU169208 AGENCOURT
5	45	90.0	206	7	CF558245 1115035C0
C 6	45	90.0	494	2	BE944702 UI-M-BH3-
C 7	45	90.0	501	2	BE949131 UI-M-BH3-
C 8	45	90.0	590	5	BQ638095 hd18d07.y
C 9	44	88.0	528	8	AQ807467 HS_3207_B

C	10	44	88.0	528	8	AQ807479	AQ807479 HS_3207_B
	11	44	88.0	699	6	BY748808	BY748808 BY748808
	12	44	88.0	846	4	BI916220	BI916220 603178115
C	13	44	88.0	1007	5	BQ439107	BQ439107 AGENCOURT
	14	43	86.0	276	2	BB608644	BB608644 BB608644
C	15	43	86.0	370	4	BG942814	BG942814 ax30a01.x
	16	43	86.0	425	1	AI552042	AI552042 mm73g06.y
	17	43	86.0	433	1	AA072623	AA072623 mm73g06.x
C	18	43	86.0	443	9	CE667699	CE667699 tigr-g88-
	19	43	86.0	498	2	AW180619	AW180619 MGA0762f
	20	43	86.0	516	6	CD217252	CD217252 TgESTzyi2
	21	43	86.0	517	5	BU699322	BU699322 LL2in1125
C	22	43	86.0	530	4	BI848950	BI848950 471549 MA
C	23	43	86.0	576	5	BX643028	BX643028 DKFZp781G
C	24	43	86.0	594	5	BP768145	BP768145 BP768145
	25	43	86.0	650	2	BB618995	BB618995 BB618995
C	26	43	86.0	652	8	BZ952846	BZ952846 CH240_125
	27	43	86.0	676	8	BH099003	BH099003 RPCI_24-3
C	28	43	86.0	714	2	BE176609	BE176609 RC3-HT058
	29	43	86.0	827	9	CL714569	CL714569 OR_BBa003
	30	43	86.0	1143	5	BQ050317	BQ050317 AGENCOURT
C	31	42	84.0	245	2	BB240512	BB240512 BB240512
	32	42	84.0	253	2	BB603301	BB603301 BB603301
	33	42	84.0	400	1	AL361639	AL361639 AL361639
	34	42	84.0	413	8	AZ141369	AZ141369 SP_0042_A
	35	42	84.0	429	8	AQ702310	AQ702310 HS_5332_B
	36	42	84.0	445	5	BY451956	BY451956 BY451956
	37	42	84.0	446	4	BM271588	BM271588 TgESTzyb4
C	38	42	84.0	446	5	BW523847	BW523847 BW523847
	39	42	84.0	452	7	CN605793	CN605793 PEL0290_P
C	40	42	84.0	476	7	CO072048	CO072048 GR_Ea31A
C	41	42	84.0	495	7	CN664303	CN664303 A0811D10-
	42	42	84.0	500	7	CN605683	CN605683 PEL0091_P
C	43	42	84.0	530	8	AQ189600	AQ189600 HS_3219_B
	44	42	84.0	537	8	BH330237	BH330237 CH230-58M
	45	42	84.0	555	4	BG883465	BG883465 fp29g12.x

ALIGNMENTS

RESULT 1
BZ178637

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BZ178637 911 bp DNA linear GSS 11-OCT-2002
CH230-456M15.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-456M15, genomic survey sequence.

BZ178637 GI:23822768

GSS.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 911)

Zhao, S., Shetty, J., Shatsman, S., Tseng, G., Geer, K.,

Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,

Riggs, F., de Jong, P., and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 MboI segment

Unpublished (1999)

Other GSSs: CH230-456M15.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fax: 301 838 0200

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 456 row: M column: 15

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers
1. .911
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SENHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-456M15"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Alignment Scores:
Pred. No.: 75.1 Length: 911
Score: 50.00 Matches: 9
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-40 (1-9) x BZ178637 (1-911)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
Db 17 GTTCTGGGTGGACTAGTCAATTGTGT 43

RESULT 2

CK375056/c

LOCUS

DEFINITION lai44c10.y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5', similar to SW:TLM_MOUSE P17408 TLM PROTEIN ;, mRNA sequence.

ACCESSION CK375056

VERSION CK375056.1 GI:40340298

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 562)
Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L., Waterston,R. and Wilson,R.

WashU Stem cell EST Project

Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett

WashU, Human Genetics Division

Washington University School of Medicine

1st strand of cDNA was synthesized with reverse transcriptase and

oligo(dT) beads, then cDNA was amplified by PCR using modified

SMART primers. The final cDNA was cloned in pAMP1 vector in

annealing reaction with Uracil DNA Glycosylase (UDG). Library

constructed by Y.Korshunova and M. Lovett. Library materials

provided by Mills JC & Gordon JI.

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gibco.

FEATURES

source

Location/Qualifiers
1. .562
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Laser-captured isthmal cells from tox176
transgenic mice"
/dev_stage="adult"
/lab_host="DH5alpha"
/clone_lib="Gastric Epithelial Progenitor 2"
/note="Vector: pAMP1; 1st strand of cDNA was synthesized

with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y.Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI."

ORIGIN

Alignment Scores:
Pred. No.: 162 Length: 562
Score: 47.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 94.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-40 (1-9) x CK375056 (1-562)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 448 CTCTTAGGGGGTCTTGGTCAATTGTGC 422

RESULT 3

CL895276/c

LOCUS

DEFINITION abg3lh01.y1 Soybean random, unfiltered genomic library Glycine max genomic, genomic survey sequence.

ACCESSION CL895276

VERSION CL895276.1 GI:51644968

KEYWORDS

SOURCE Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 415)

REFERENCE

AUTHORS

Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J., Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and Stacey,G.

Methylation filtered genomic sequences from Glycine max

Unpublished (2004)

TITLE

JOURNAL

COMMENT

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-1267

Fax: 573-882-0588

Email: staceyg@missouri.edu

Lidid: 230

FEATURES

source

Location/Qualifiers
1. .415
/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 230"

ORIGIN

Alignment Scores:
Pred. No.: 179 Length: 415
Score: 46.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-40 (1-9) x CL895276 (1-415)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 267 TTGGGGGGACTTGGTCAATTTTGC 244

RESULT 4
BUI69208
LOCUS
DEFINITION BUI69208 951 bp mRNA linear EST 04-SEP-2002
5', mRNA sequence. AGENCOURT_8099372 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6254236
ACCESSION BUI69208
VERSION BUI69208.1 GI:22683192
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT 1 (bases 1 to 951)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2403 row: g column: 05
High quality sequence start: 23
High quality sequence stop: 735.
Location/Qualifiers

FEATURES
source
1..951
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6254236"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 436 Length: 951
Score: 46.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x BUI69208 (1-951)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 916 TTGGGGGGCCTTGGCAATTTTGC 939

RESULT 5
CF558245
LOCUS
DEFINITION CF558245 206 bp mRNA linear EST 23-SEP-2003
1115035C04.x2 C. reinhardtii CC-1690 (mt+), Stress III
(normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA
sequence.
ACCESSION CF558245

VERSION CF558245.1 GI:34984328
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 206)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
Merchant,S., Quinn,J. and Shrager,J.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1115
JOURNAL Unpublished (2003)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
High quality sequence stop: 206.
Location/Qualifiers

FEATURES
source
1..206
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III
(normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition III library, constructed by
Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from
CC-1690 cells grown to mid-log phase in copper-free TAP
medium (see Quinn and Merchant (1998) Methods in
Enzymology, 2997:263-279) in a shaking (250 rpm) illuminated
(about 100 micromole/m2/sec) incubator at 22 C (see Quinn
and Merchant (1998) Methods in Enzymology, 2997:263-279);
CC-1690 cells grown to mid-log phase in low Fe (1
micromolar Fe) TAP medium (see La Fontaine S, Quinn JM,
Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J,
Merchant S.LaFontaine et al. (2002) Eukaryotic Cell,
1:736-757) in a shaking illuminated incubator (same
conditions as above). CC-1690 cells were grown to mid-log
phase in TAP medium in a shaking illuminated incubator to
a density of 8x10e6 cells/ml. The flask was transferred to
a shaking platform (200 rpm) at room temperature (23C) 12
micromole/m2/sec illumination and bubbled in a stoppered
flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour
prior to harvesting for RNA isolation (as per Quinn JM,
Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC
275:6080-6089); CC-1690 cells grown to mid-log phase
(3x10e6 cells/ml) in TAP medium in a shaking (150 rpm)
illuminated (70 mole photon/m2/sec) incubator at 27 C.
Cells were diluted to 1x10e6 cells/ml, transferred to high
light (11000 mol photon/m2/s) with shaking (150 rpm) and
sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to
mid-log phase in HS medium in a shaking (150 rpm)
illuminated (70 mole photon/m2/sec) incubator at 27 C.
Cells were diluted to 1x10e6 cells/ml, transferred to high
light (11000 mol photon/m2/s) with shaking (150 rpm) and
sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified
from each sample, pooled and cDNA synthesized (see Shrager
et al, Plant Physiol. 131, 401-408 for details). The cDNA
was directionally cloned into lambda Zap II (Stratagene)
in the EcoRI (5') and XhoI (3') sites. pBluescript II SK-
plasmids were excised from the lambda Zap clones by
superinfection with ExAssist (Stratagene) phage. The
library was normalized using method 4 described in Bonaldo
et al., (1996) Genome Research 6: 791-806."

ORIGIN

Alignment Scores:
Pred. No.: 130 Length: 206

Score: 45.00 Matches: 7
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 0
Query Match: 90.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-40 (1-9) x CF558245 (1-206)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|||||:::|||||:::|||||

Db 156 ATCCTGGGGGATTGGGGCGGTCTTGC 182

RESULT 6
BE944702/c

LOCUS BE944702 494 bp mRNA linear EST 03-OCT-2000
DEFINITION UI-M-BH3-awg-a-04-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
ACCESSION BE944702
VERSION BE944702.1 GI:10522461
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 494)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEst@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
olfactory bulbs tissue cDNA Library Preparation: M.B. Soares Lab
Clone distribution: Researchers may obtain BMAP cDNA clones from
RESEARCH GENETICS. It should be noted that Bento Soares is
generating a small number of additional specialized non-redundant
arrays of BMAP cDNAs whose availability will be considered under
appropriate and limited collaborative arrangements The following
repetitive elements were found in this cDNA sequence: 265-494,
>MTD#LTR/MaLR
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source Location/Qualifiers
1. .494
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH3-awg-a-04-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries

were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_TISSUE=olfactory-bulbs
TAG_LIB=NIH_BMAP_M_S4
TAG_SEQ=CAAGG"

ORIGIN

Alignment Scores: 332 Length: 494
Pred. No.: 45.00 Matches: 8
Score: 88.89% Conservative: 0
Percent Similarity: 88.89% Mismatches: 1
Best Local Similarity: 90.00% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-10-014-101B-40 (1-9) x BE944702 (1-494)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||

Db 238 GTGTTAGGGGTTTGGGGGATTTTGT 212

RESULT 7
BE949131/c

LOCUS BE949131 501 bp mRNA linear EST 03-OCT-2000
DEFINITION UI-M-BH3-avh-e-05-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
ACCESSION BE949131
VERSION BE949131.1 GI:10526890
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 501)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEst@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
olfactory bulbs tissue cDNA Library Preparation: M.B. Soares Lab
Clone distribution: Researchers may obtain BMAP cDNA clones from
RESEARCH GENETICS. It should be noted that Bento Soares is
generating a small number of additional specialized non-redundant
arrays of BMAP cDNAs whose availability will be considered under
appropriate and limited collaborative arrangements The following
repetitive elements were found in this cDNA sequence: 265-501,

FEATURES

source

>MTD#LTR/MaLR

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. .501

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-BH3-avh-e-05-0-UI"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH_BMAP_M_S4"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_TISSUE=olfactory-bulbs

TAG_LIB=NIH_BMAP_M_S4

TAG_SEQ=CATGG

FEATURES

source

Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts

Mol. Vis. 8 (4), 196-204 (2002)

22103461

12107411

COMMENT

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 18 row: d column: 07

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1. .590

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="hd18d07"

/tissue_type="Retina"

/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="Human Retina cDNA (Un-normalized, unamplified): hd/he"

/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor

[5'-pGACTAGTTCATGATCGGCGGCCGCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.: 337 Length: 501

Score: 45.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 90.00% Indels: 0

DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x BE949131 (1-501)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 238 GTGTTAGGGGTTGGGGGATTTTGT 212

RESULT 8

BQ638095/c

LOCUS

DEFINITION

hdi8d07.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he

Homo sapiens cDNA clone hdi8d07 5', mRNA sequence.

ACCESSION

BQ638095

VERSION

BQ638095.1 GI:21762554.

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 590)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

ORIGIN

Alignment Scores:

Pred. No.: 401 Length: 590

Score: 45.00 Matches: 7

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 77.78% Mismatches: 0

Query Match: 90.00% Indels: 0

DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x BQ638095 (1-590)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

Db 115 ATCCTTGGGGCCTGGGGAATTTGT 89

RESULT 9

AQ807467/c

LOCUS

DEFINITION

AQ807467

sapiens genomic clone Plate=3207 Col=7 Row=F, genomic survey sequence.

ACCESSION

AQ807467

VERSION

AQ807467.1 GI:5726709

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 528)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3207 row: F column: 7
Seq primer: T7
Class: BAC ends
High quality sequence stop: 528.
Location/Qualifiers
1. .528
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3207 Col=7 Row=F"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

FEATURES
source
1. .528
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3207 Col=7 Row=F"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Alignment Scores:
Pred. No.: 547 Length: 528
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 8 Gaps: 0
US-10-014-101B-40 (1-9) x AQ807467 (1-528)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
:::|||||
Db 506 ATAGGTGGGCTGGGGCAATTCTGT 483

RESULT 10
AQ807479/c
LOCUS HS_3207_B1_D04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=7 Row=H, genomic survey sequence.
DEFINITION AQ807479 528 bp DNA linear GSS 10-AUG-1999
ACCESSION AQ807479.1 GI:5726721
VERSION
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3207 row: H column: 7
Seq primer: T7
Class: BAC ends
High quality sequence stop: 528.
Location/Qualifiers
1. .528
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3207 Col=7 Row=H"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

FEATURES
source
1. .528
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3207 Col=7 Row=H"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Alignment Scores:
Pred. No.: 547 Length: 528
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 8 Gaps: 0
US-10-014-101B-40 (1-9) x AQ807479 (1-528)

Qy 2 LeuGlyGlyLeuGlyGlnPheCys 9
:::|||||
Db 506 ATAGGTGGGCTGGGGCAATTCTGT 483

RESULT 11
BY748808
LOCUS BY748808 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630207H20 5', mRNA sequence.
DEFINITION BY748808 699 bp mRNA linear EST 17-DEC-2002
ACCESSION BY748808
VERSION BY748808.1 GI:27177838
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 699)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasai,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Salto, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES source Location/Qualifiers
1. .699
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630207H20"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

ORIGIN
Alignment Scores:
Pred. No.: 739 Length: 699
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-40 (1-9) x BY748808 (1-699)
QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||:|||||
Db 526 CTGGGAGGATGGGCGAGTTTGT 549
RESULT 12
BI916220
LOCUS BI916220 846 bp mRNA linear EST 17-OCT-2001
DEFINITION 603178115F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242539 5',

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Salto, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES source Location/Qualifiers
1. .699
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630207H20"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

ORIGIN
Alignment Scores:
Pred. No.: 739 Length: 699
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-40 (1-9) x BY748808 (1-699)
QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||:|||||
Db 526 CTGGGAGGATGGGCGAGTTTGT 549
RESULT 12
BI916220
LOCUS BI916220 846 bp mRNA linear EST 17-OCT-2001
DEFINITION 603178115F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242539 5',

ACCESSION BI916220

VERSION BI916220.1 GI:16199430

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 846)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1611 row: m column: 04
High quality sequence stop: 239.
Location/Qualifiers
1. .846
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5242539"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 906 Length: 846
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-40 (1-9) x BI916220 (1-846)
QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||:|||||
Db 542 CTAGGGGTATAGGCCAATTCGTC 565
RESULT 13
BQ439107/c
LOCUS BQ439107 1007 bp mRNA linear EST 24-MAY-2002
DEFINITION BQ439107 1007 bp Homo sapiens cDNA clone IMAGE:6024189 5', mRNA sequence.
ACCESSION BQ439107
VERSION BQ439107.1 GI:21178183
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1007)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13234 row: e column: 22
High quality sequence stop: 484.
Location/Qualifiers
1. .1007
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6024189"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

FEATURES

source

FEATURES

source

Location/Qualifiers

1. .276
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E330007A21"
/sex="female"
/tissue_type="ovary"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 2 days pregnant adult female ovary"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGAGAGACGGCGCAACTCGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Alignment Scores:
Pred. No.: 1.09e+03 Length: 1007
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 0
Query Match: 88.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x BQ439107 (1-1007)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
||||:|||||||:|||||:|||||
Db 711 GTTATTGGGGTCTTGGCGTTTCTGC 685

RESULT 14

BB608644

LOCUS

DEFINITION BB608644 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330007A21 5', mRNA sequence.

ACCESSION BB608644

VERSION BB608644.1 GI:11563821

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 276)

REFERENCE

AUTHORS

Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoiyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>

ORIGIN

Alignment Scores:
Pred. No.: 419 Length: 276
Score: 43.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x BB608644 (1-276)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||:|||||:|||||:|||||

Db 225 GTCTTTGGGGTCTAGGTGAATCTGT 251

RESULT 15

BB942814/c

LOCUS

DEFINITION BB942814 370 bp mRNA linear EST 15-JAN-2003 ax30a01.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library)
Homo sapiens cDNA clone ax30a01 random, mRNA sequence.

ACCESSION BB942814

VERSION BB942814.1 GI:14342186

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 370)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells

JOURNAL Genomics 59 (2), 168-177 (1999)
MEDLINE 99339981
PUBMED 10409428
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jm7f@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 30 row: a column: 01
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. .370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ax30a01"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax
library)"
/note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using TRIzol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's CapFinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH intramural sequencing center
http://www.nisc.nih.gov/)."

ORIGIN
Alignment Scores:
Pred. No.: 573 Length: 370
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-40 (1-9) x BG942814 (1-370)
Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 75 GTTCTGGGTGGCCTGGGCTGTTCTGC 49
RESULT 16
AI552042
LOCUS AI552042 425 bp mRNA linear EST 15-MAR-2000
DEFINITION mm73g06.y1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
clone IMAGE:534106 5', mRNA sequence.
ACCESSION AI552042
VERSION AI552042.1 GI:4484405
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
MGI:321042
Seq primer: -40RP from Gibco
High quality sequence stop: 395
POLYA=No.

FEATURES
source Location/Qualifiers
1. .425
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:534106"
/tissue_type="macrophage"
/dev_stage="WEHI-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse macrophage (#937306)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTGGCAGCAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN
Alignment Scores:
Pred. No.: 665 Length: 425
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 1 Gaps: 0
US-10-014-101B-40 (1-9) x AI552042 (1-425)
Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 280 GTACTGGGAGGCTTGGGTTGTTTTC 306
RESULT 17
AA072623
LOCUS AA072623 433 bp mRNA linear EST 07-FEB-1997
DEFINITION mm73g06.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
clone IMAGE:534106 5', mRNA sequence.
ACCESSION AA072623
VERSION AA072623.1 GI:1594354
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project

REFERENCE
AUTHORS
1 (bases 1 to 425)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
MGI:321042
Seq primer: -40RP from Gibco
High quality sequence stop: 395
POLYA=No.

FEATURES
source Location/Qualifiers
1. .425
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:534106"
/tissue_type="macrophage"
/dev_stage="WEHI-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse macrophage (#937306)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTGGCAGCAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN
Alignment Scores:
Pred. No.: 665 Length: 425
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 1 Gaps: 0
US-10-014-101B-40 (1-9) x AI552042 (1-425)
Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 280 GTACTGGGAGGCTTGGGTTGTTTTC 306
RESULT 17
AA072623
LOCUS AA072623 433 bp mRNA linear EST 07-FEB-1997
DEFINITION mm73g06.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
clone IMAGE:534106 5', mRNA sequence.
ACCESSION AA072623
VERSION AA072623.1 GI:1594354
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project

US-10-014-101B-40 (1-9) x AW180619 (1-498)			
QY	1	ValLeuGlyGlyLeuGlyGlnPheCys 9	
Db	108	GTACTTGGAGGTATCGGTCAATTTTGC 82	
RESULT 20			
CD217252			
LOCUS	CD217252	516 bp	linear mRNA EST 20-MAY-2003
DEFINITION	TgESTzyi22b05.y1 TgMAS tachyzoite cDNA Library Toxoplasma gondii		
	CDNA clone TgESTzyi22b05.y1 5' similar to SW:RL39_HUMAN P02404 60S		
	RIBOSOMAL PROTEIN L39. ;, mRNA sequence.		
ACCESSION			
VERSION	CD217252		
KEYWORDS	EST.		
SOURCE	Toxoplasma gondii		
ORGANISM	Toxoplasma gondii		
REFERENCE			
AUTHORS	Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioke,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.		
	Toxoplasma EST Project		
	Unpublished (2001)		
	Contact: Clifton, S.		
	Toxoplasma EST Project		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: toxo@watson.wustl.edu		
	Contact David Sibley (toxoeest@borcim.wustl.edu) for further		
	information relating to organism, libraries, or clone availability.		
	Possible reversed clone: similarity on wrong strand		
	Seq primer: -40RP from Gibco.		
FEATURES			
	source	Location/Qualifiers	
	1..516	/organism="Toxoplasma gondii"	
		/mol_type="mRNA"	
		/strain="Tachyzoite"	
		/db_xref="taxon:5811"	
		/clone="TgESTzyi22b05.y1"	
		/dev_stage="Tachyzoite"	
		/lab_host="ElectroTen Blue cells (Stratagene)"	
		/clone_lib="TgMAS Tachyzoite cDNA Library"	
		/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by Keliang Tang, and Robert Cole at Washington University. cDNA was synthesized from Poly(A)+ mRNA using an oligo-d(T) primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/XhoI prepared pBluescript II SK+ vector, and electroporated into ElectroTen Blue cells (Stratagene). The library may contain a small percentage of host or bacterial contaminants."	
ORIGIN			
Alignment Scores:			
Pred. No.:	819	Length:	516
Score:	43.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	3
Best Local Similarity:	66.67%	Mismatches:	0
Query Match:	86.00%	Indels:	0
DB:	6	Gaps:	0
US-10-014-101B-40 (1-9) x CD217252 (1-516)			
QY	1	ValLeuGlyGlyLeuGlyGlnPheCys 9	
Db	108	GTACTTGGAGGTATCGGTCAATTTTGC 82	
RESULT 21			
BU699322			
LOCUS	BU699322	517 bp	linear mRNA EST 09-OCT-2002
DEFINITION	LL2ini11254T7 Hematopoietic Stem Cell Subtracted Library Mus		
	musculus cDNA 5', mRNA sequence.		
ACCESSION			
VERSION	BU699322.1	GI:23615910	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	1 (bases 1 to 517)		
	Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.		
	The genetic program of hematopoietic stem cells		
	Science 288 (5471), 1635-1640 (2000)		
	20295303		
	10834841		
	Contact: Lemischka, Ihor R.		
	Department of Molecular Biology		
	Princeton University		
	Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA		
	Tel: 609 258 2838		
	Fax: 609 258 2759		
	Email: ilemischka@molbio.princeton.edu		
	These ESTs are derived from a subtracted cDNA library enriched for		
	gene products expressed in day 14-14.5 fetal liver hematopoietic		
	stem cells defined as Lineageneg/lo, AA4.lpos, cKitpos, Ly6A/E		
	(Sca-1)pos		
	Seq primer: M13Reverse or T7.		
FEATURES			
	source	Location/Qualifiers	
	1..517	/organism="Mus musculus"	
		/mol_type="mRNA"	
		/strain="C57BL/6J"	
		/db_xref="taxon:10090"	
		/tissue_type="Hematopoietic"	
		/cell_type="Stem Cells; Lineageneg/lo, AA4.lpos, cKitpos, Ly6A/E (Sca-1)pos"	
		/dev_stage="Embryonic day 14-14.5"	
		/lab_host="DH10B"	
		/clone_lib="Hematopoietic Stem Cell Subtracted Library"	
		/note="Organ: Fetal Liver; Vector: Sport 1; Site 1: Sal I; Site 2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.lpos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.lneg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.lneg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."	
ORIGIN			
Alignment Scores:			
Pred. No.:	821	Length:	517
Score:	43.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	86.00%	Indels:	0
DB:	5	Gaps:	0
US-10-014-101B-40 (1-9) x BU699322 (1-517)			
QY	1	ValLeuGlyGlyLeuGlyGlnPheCys 9	
Db	111	GTACTGGAGGCTTGGGTTTGTTC 137	

RESULT 22
BI848950/c
LOCUS
DEFINITION 471549 MARC 2BOV Bos taurus cDNA 5', mRNA linear EST 04-OCT-2001
ACCESSION BI848950
VERSION BI848950.1 GI:15961469
KEYWORDS
SOURCE
ORGANISM Bos taurus (cow)

REFERENCE
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
Plate: 99 row: A column: 8
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source
1..530
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

ORIGIN
Alignment Scores:
Pred. No.: 843 Length: 530
Score: 43.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x BI848950 (1-530)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::||||| |||||
Db 335 ATCCTTGGAGCCCTGGGTCAgTTCTGT 309

RESULT 23
BX643028/c
LOCUS
DEFINITION DKFZp781G0822_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
ACCESSION BX643028
VERSION BX643028.1 GI:34477361

KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS 1 (bases 1 to 576)
Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp781G0822) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..576
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp781G0822"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN
Alignment Scores:
Pred. No.: 921 Length: 576
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 86.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x BX643028 (1-576)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 103 GTTCTGGTGGCTGGGCTGTCTGTC 77

RESULT 24
BP768145/c
LOCUS
DEFINITION BP768145 mouse (C57BL/6) pancreatic islet library with recombination-based method Mus musculus cDNA clone mid30071 3', mRNA sequence.
ACCESSION BP768145
VERSION BP768145.1 GI:50226843
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 594)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H., Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360

Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.

FEATURES

source

Location/Qualifiers
1. .594
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mid30071"
/sex="male"
/tissue_type="pancratic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with recombination-based method"

ORIGIN

Alignment Scores: 952 Length: 594
Pred. No.: 43.00 Matches: 7
Score: 100.00%
Percent Similarity: 87.50%
Best Local Similarity: 86.00%
Query Match: 5
DB: 0

US-10-014-101B-40 (1-9) x BP768145 (1-594)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9

|||||:::|||||

Db 522 TTGGTGGTGTGGTCAGTTTGT 499

RESULT 25

BB618995

LOCUS

DEFINITION

BB618995 RIKEN full-length enriched, 8 days embryo Mus musculus
CDNA clone 5730462C14 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 650)

REFERENCE

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physiscal and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

1. .650

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="5730462C14"

/sex="mixed"

/dev_stage="8 days embryo"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 8 days embryo"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',

GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

ORIGIN

Alignment Scores:

Pred. No.: 1.05e+03 Length: 650
Score: 43.00 Matches: 8
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 86.00%
DB: 2
Gaps: 0

US-10-014-101B-40 (1-9) x BB618995 (1-650)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

|||||

Db 11 GTCTCGGGCGCCTGGGTGGCTTCTGC 37

RESULT 26

BB618995

LOCUS

DEFINITION

BB618995 RIKEN full-length enriched, 8 days embryo Bos taurus genomic clone CH240_125L7, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 652)
Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=RC3-HT0585-010
400-023-h11&t3=2000-04-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 45
High quality sequence stop: 685.

FEATURES

source

1. .714
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0585"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	1.16e+03	Length:	714
Score:	43.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	87.50%	Mismatches:	0
Query Match:	86.00%	Indels:	0
DB:	2	Gaps:	0

US-10-014-101B-40 (1-9) x BE176609 (1-714)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9

|||||:::|||||

Db 57 CTAGGAGGAGTAGGGCAGTTCTGC 34

RESULT 29

CL714569

LOCUS

DEFINITION OR_BB0039F11.r OR_BB0 Oryza rufipogon genomic clone OR_BB0039F11
3', genomic survey sequence.

ACCESSION CL714569

VERSION CL714569.1 GI:50601607

KEYWORDS GSS.

SOURCE

ORGANISM

Oryza rufipogon

Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 827)

Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,

Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

OMAP Project

Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: http://genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161 Std Error: 0.00

Plate: 0039 row: F column: 11

Seq primer: CAC TCA TTA GGC ACC CCA

Class: BAC ends.

FEATURES

source

1. .827

Location/Qualifiers

/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BB0039F11"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Alignment Scores:

Pred. No.:	1.36e+03	Length:	827
Score:	43.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	77.78%	Mismatches:	0
Query Match:	86.00%	Indels:	0
DB:	9	Gaps:	0

US-10-014-101B-40 (1-9) x CL714569 (1-827)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9

|||||:::|||||

Db 459 GTCGTAGGAGGTCTCGGAAGGTTTGT 485

RESULT 30

BQ050317

LOCUS

DEFINITION BQ050317 1143 bp mRNA linear EST 29-MAR-2002
AGENCOURT_7050735 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784242
5', mRNA sequence.

ACCESSION BQ050317

VERSION BQ050317.1 GI:19809657

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1143)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12869 row: h column: 03

High quality sequence stop: 525.

FEATURES

source

1. 1143
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5784242"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN

Alignment Scores:

Pred. No.:	1.92e+03	Length:	1143
Score:	43.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	87.50%	Mismatches:	0
Query Match:	86.00%	Indels:	0
DB:	5	Gaps:	0

19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES
source
1. .253
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D830007B12"
/tissue_type="heart"
/dev_stage="16 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 16 days neonate heart"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGAGAGAGCGGCCGAACCTCGAGTTTTTTTTTTTTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGAGATTCTCGAGTTAATAATATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN
Alignment Scores:
Pred. No.: 586 Length: 253
Score: 42.00 Matches: 6
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-40 (1-9) x BB603301 (1-253)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|||||:::|||||

Db 191 ATCTTTGGGGTCTAGGTGAATTCGT 217

RESULT 33
AL361639 400 bp mRNA linear EST 04-AUG-2000
LOCUS
DEFINITION
mRNA sequence.
ACCESSION
AL361639.1 GI:9692561
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 400)
Eickhoff,H., Schuchhardt,J., Ivanov,I., Meier-Ewert,S., O'Brien,J., Malik,A., Tandon,N., Wolski,E., Rohlfis,E., Nyarsik,L., Reinhardt,R., Nietfeld,W. and Lehrach,H.
Tissue gene expression analysis using arrayed normalized cDNA libraries
Genome Res. (2000) In press
Contact: MPING
Abt.Lehrach
Max Planck Institut Fuer Molekulare Genetik
Innestrasse 73, Berlin, 14195 Germany
The cDNA libraries ICRFp 522 and 523 were normalized with oligonucleotide fingerprinting, resulting in a unique subset of 5376 cDNA clones.

FEATURES
source
Location/Qualifiers
1. .400

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="M9129A60"
/tissue_type="embryo"
/dev_stage="9 and 12 pc embryo"
/clone_lib="ICRFp 522 and 523"

ORIGIN
Alignment Scores:
Pred. No.: 957 Length: 400
Score: 42.00 Matches: 6
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-40 (1-9) x AL361639 (1-400)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|||||:::|||||

Db 310 ATAATCGGAGATTGGGCAGTTCTGT 336

RESULT 34
AZ141369
LOCUS
DEFINITION
SP_0042_A1_C10_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=42 Col=19 Row=E, genomic survey sequence.
ACCESSION
AZ141369.1 GI:8293272
VERSION
KEYWORDS
SOURCE
Strongylocentrotus purpuratus
ORGANISM
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
REFERENCE
1 (bases 1 to 413)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
10920195
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 42 row: E column: 19
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 413.
Location/Qualifiers
1. .413
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="Plate=42 Col=19 Row=E"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACE3.6; BAC Clones in E-Coli DH10B"

ORIGIN
Alignment Scores:
Pred. No.: 990 Length: 413

Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-40 (1-9) x AZ141369 (1-413)

QY 2 LeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 109 TTGGAGGCCTTGAAGGTTTGT 132
|||||

RESULT 35

AQ702310

LOCUS

DEFINITION

HS_5332 B1 D11 T7A RPCI-11 Human Male BAC Library Homo sapiens

genomic clone Plate=908 Col=21 Row=H, genomic survey sequence.

ACCESSION

AQ702310

VERSION

AQ702310.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 429)

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL

MEDLINE

PUBMED

99380589

10449764

CONTACT: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 908 row: H column: 21

Seq primer: T7

Class: BAC ends

High quality sequence stop: 429.

Location/Qualifiers

1..429

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=908 Col=21 Row=H"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACe3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:

Pred. No.: 1.03e+03

Score: 42.00 Length: 429

Percent Similarity: 88.89% Matches: 7

Best Local Similarity: 77.78% Conservative: 1

Query Match: 84.00% Mismatches: 1

DB: 8 Indels: 0

Gaps: 0

US-10-014-101B-40 (1-9) x AQ702310 (1-429)

QY 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|||||
Db 90 CTCCTCGGGGGGCTTGGGATGTTCTGC 116
|||||

RESULT 36

BY451956

LOCUS

DEFINITION

BY451956 RIKEN full-length enriched, pooled tissues, adult spleen,

etc. Mus musculus cDNA clone K630057J12 3', mRNA sequence.

ACCESSION

BY451956

VERSION

BY451956.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 445)

AUTHORS

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,

Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kwasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Perte,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shinada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,

Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL

MEDLINE

PUBMED

12466851

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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/

Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,

Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,

Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and

Hayashizaki,Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
source

Location/Qualifiers
1. .445
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K630057J12"
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."
/note="(dev_stage=adult,tissue_type=spleen,sex=male), (dev_stage=adult,tissue_type=kidney,sex=male), (dev_stage=adult,tissue_type=testis,sex=male), (dev_stage=adult,tissue_type=thymus,sex=male), (dev_stage=adult,tissue_type=heart,sex=male), (dev_stage=adult,tissue_type=colon,sex=male), (dev_stage=adult,tissue_type=stomach,sex=male), (dev_stage=adult,tissue_type=liver,sex=male), (dev_stage=13 days embryo,tissue_type=whole body,sex=mix), (dev_stage=14 days embryo,tissue_type=whole body,sex=mix), (dev_stage=16 days embryo,tissue_type=whole body,sex=mix), (dev_stage=17 days embryo,tissue_type=whole body,sex=mix), (dev_stage=15 days pregnant, adult,tissue_type=amnion,sex=female), (dev_stage=10 days neonate,tissue_type=brain,sex=mix), (dev_stage=10 days neonate,tissue_type=thymus,sex=mix), (dev_stage=10 days neonate,tissue_type=heart,sex=mix)"

ORIGIN

Alignment Scores:

Pred. No.: 1.07e+03 Length: 445
Score: 42.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x BY451956 (1-445)

Qy 3 GlyGlyLeuGlyGlnPheCys 9
|||||
Db 127 GGGGGGCTGGTCAGTTTGC 147

RESULT 37

BM271588

LOCUS

DEFINITION BM271588 446 bp mRNA linear EST 20-DEC-2001
TgESTzyb49c11.y2 TgrH Tachyzoite Subtracted cDNA Library Toxoplasma gondii cDNA clone TgESTzyb49c11.y2 5', mRNA sequence.

ACCESSION BM271588

VERSION BM271588.1 GI:17964860

KEYWORDS EST.

SOURCE

ORGANISM

Toxoplasma gondii

Toxoplasma gondii

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Toxoplasma.

1 (bases 1 to 446)

REFERENCE
AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.

Toxoplasma EST Project

Unpublished (2001)

JOURNAL Contact: Clifton, S.

COMMENT Toxoplasma EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 421.

FEATURES

source

Location/Qualifiers
1. .446
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/strain="RH (Type I)"
/db_xref="taxon:5811"
/clone="TgESTzyb49c11.y2"
/dev_stage="Tachyzoite"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="TgrH Tachyzoite Subtracted cDNA Library"
/note="Vector: pBluscript SK-; Site 1: EcoRI; Site 2: XhoI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L.Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the Lambda ZapII vector using the Zap-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using ExAssist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of over-represented ESTs (N>=12, from 5596 previous reads). The subtracted library was electroporated into DH10B (GeneHog, Invitrogen, Inc). WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library Source: David Sibley, Washington University."

ORIGIN

Alignment Scores:
Pred. No.: 1.08e+03 Length: 446
Score: 42.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-40 (1-9) x BM271588 (1-446)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|||||
Db 39 CTCTAGGAGGACTTGGTAACCTCTGT 65

RESULT 38

BM523847/c

LOCUS

DEFINITION BM523847 Yutaka Satou unpublished cDNA library (csga) Ciona savignyi cDNA clone csga085gl7 5', mRNA sequence.

ACCESSION BM523847

VERSION BM523847.1 GI:51685545

KEYWORDS EST.

SOURCE

ORGANISM

Ciona savignyi

Ciona savignyi

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 446)

REFERENCE
AUTHORS Satou,Y. and Satoh,N.

TITLE Expressed genes in Ciona savignyi

JOURNAL Unpublished (2004)

COMMENT Contact: Yutaka Satou

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4095

Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers

FEATURES
source

1. .446
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="csga085g17"
/dev_stage="gastrula stage"
/clone_lib="Yutaka Satou unpublished cDNA library (csga)"

ORIGIN

Alignment Scores:
Pred. No.: 1.08e+03 Length: 446
Score: 42.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-40 (1-9) x BW523847 (1-446)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
|||||
Db 69 GTGCTTGAGGATTGGGAGGTTTGT 43

RESULT 39

CN605793
LOCUS
DEFINITION
CN605793 452 bp mRNA linear EST 30-SEP-2004
PEL0290 Primordial expressed cDNA library lambda ZAP Lentinula
edodes cDNA clone PEL0290 3' similar to 60S ribosomal protein L30
(S. pombe), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Lentinula edodes (shiitake mushroom)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Lentinula.
1 (bases 1 to 452)
Ng,T.P., Bian,X.L., Ng,W.L. and Kwan,H.S.
Expressed Sequence Tags from Lentinula edodes
Unpublished (2004)

Contact: Kwan, H.S.
Food and Nutritional Sciences Programme, Molecular Biotechnology
Programme, Department of Biology
The Chinese University of Hong Kong
Science Centre, Shatin, N.T., Hong Kong SAR
Tel: 852-26096285
Fax: 852-26035745
Email: hoishankwan@cuhk.edu.hk
PCR Primers
FORWARD: T3
BACKWARD: T7
Insert Length: 452 Std Error: 0.00
Seq primer: Oligo dT25N
POLYA=No.

FEATURES
source

1. .452
/organism="Lentinula edodes"
/mol_type="mRNA"
/strain="L54"
/db_xref="taxon:5353"
/clone="PEL0290"
/sex="Dikaryon"
/dev_stage="Primordium"
/clone_lib="Primordial expressed cDNA library lambda ZAP"
/note="Vector: lambda ZAP Express(TM) vector (Stratagene);
Site 1: EcoRI; Site 2: EcoRI; Vegetative mycelium strain
L54 was cultivated in sawdust medium. Primordium was
stimulated by induction of cold shock. mRNA from
primordium was extracted. The subsequently synthesized
cDNA library was cloned into ZAP Express(TM)

ORIGIN
vector(Stratagene)."

Alignment Scores:
Pred. No.: 1.09e+03 Length: 452
Score: 42.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-40 (1-9) x CN605793 (1-452)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|||||
Db 385 ATTCTTGGCGCCTTGGACTTTTGT 411

RESULT 40

CO072048/c
LOCUS
DEFINITION
CO072048 476 bp mRNA linear EST 15-JUN-2004
GR_Ea31A03.f GR_Ea Gossypium raimondii cDNA clone GR_Ea31A03 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CO072048
CO072048.1 GI:48741529
EST.
Gossypium raimondii
Gossypium raimondii

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 476)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 31 row: A column: 03.

FEATURES
source

1. .476
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Ea31A03"
/tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_lib="GR_Ea"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Alignment Scores:
Pred. No.: 1.15e+03 Length: 476
Score: 42.00 Matches: 6
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 84.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-40 (1-9) x CO072048 (1-476)

Qy 1 ValLeuGlyGlyLeuGlyGlnPheCys 9
:::|
Db 387 ATCATGGGGGCTTGGGCAATTTTGC 361

Search completed: February 18, 2005, 07:00:58
Job time : 1069.28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2005, 21:59:48 ; Search time 822.72 Seconds
(without alignments)
353.378 Million cell updates/sec

Title: US-10-014-101B-41
Perfect score: 27
Sequence: 1 ITRARI 6

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US10014101/runat_16022005_075845_7936/app_query.fasta_1.796
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101_QCGN_1_1_2886 @runat_16022005_075845_7936 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	100.0	111	12 SYNMRNA03	M22020 Synthetic 0
2	27	100.0	130	11 BV079618	BV079618 E2M2-130
3	27	100.0	151	8 HVU234763	AJ234763 Hordeum v
4	27	100.0	159	6 AX935409	AX935409 Sequence

C 5	27	100.0	192	6 CQ648448	CQ648448 Sequence
C 6	27	100.0	195	6 CQ651934	CQ651934 Sequence
C 7	27	100.0	195	6 AX607583	AX607583 Sequence
C 8	27	100.0	372	8 AF490285	AF490285 Phytophth
C 9	27	100.0	372	8 AF490286	AF490286 Phytophth
C 10	27	100.0	393	3 AF408671	AF408671 Trichogra
C 11	27	100.0	395	3 AF408673	AF408673 Trichogra
C 12	27	100.0	397	3 AF408672	AF408672 Trichogra
C 13	27	100.0	488	11 G58417	G58417 SHGC-104567
C 14	27	100.0	493	6 CQ476090	CQ476090 Sequence
C 15	27	100.0	540	9 HSA332323	AJ332323 Homo sapi
C 16	27	100.0	546	8 AY191142	AY191142 Oryza sat
C 17	27	100.0	547	8 AY191137	AY191137 Pyricularia
C 18	27	100.0	555	11 AF096559	AF096559 Rattus no
C 19	27	100.0	601	11 BV192133	BV192133 sqmml7346
C 20	27	100.0	648	4 AF232017	AF232017 Tamandua
C 21	27	100.0	700	3 AY330210	AY330210 Toxoplasma
C 22	27	100.0	724	9 HSA327616	AJ327616 Homo sapi
C 23	27	100.0	730	3 AY330204	AY330204 Neospora
C 24	27	100.0	800	4 AJ606422	AJ606422 Marmosops
C 25	27	100.0	805	8 AF534679	AF534679 Pyricularia
C 26	27	100.0	816	8 ZMU82201	U82201 Zea mays pa
C 27	27	100.0	860	11 BV065128	BV065128 S212P6051
C 28	27	100.0	872	8 AK103395	AK103395 Oryza sat
C 29	27	100.0	874	6 BD275463	BD275463 47 Human
C 30	27	100.0	887	11 CNS06ELJ	AL395261 T7 end of
C 31	27	100.0	900	6 E16279	E16279 gDNA encodi
C 32	27	100.0	984	4 AF434177	AF434177 Thylamys
C 33	27	100.0	984	6 AX935448	AX935448 Sequence
C 34	27	100.0	985	4 AF434176	AF434176 Thylamys
C 35	27	100.0	987	6 AX935453	AX935453 Sequence
C 36	27	100.0	987	6 AX935455	AX935455 Sequence
C 37	27	100.0	988	4 AF431925	AF431925 Thylamys
C 38	27	100.0	990	4 AF431923	AF431923 Thylamys
C 39	27	100.0	1039	6 CQ497388	CQ497388 Sequence
C 40	27	100.0	1045	3 AY333784	AY333784 Toxoplasma
C 41	27	100.0	1059	13 AY487468	AY487468 Unculture
C 42	27	100.0	1089	3 AF459563	AF459563 Drosophil
C 43	27	100.0	1098	3 AF459564	AF459564 Drosophil
C 44	27	100.0	1099	3 AF459545	AF459545 Drosophil
C 45	27	100.0	1099	3 AF459546	AF459546 Drosophil

ALIGNMENTS

RESULT 1	SYNMRNA03/c	111 bp	mRNA	linear	SYN 27-APR-1993
LOCUS	SYNMRNA03				
DEFINITION	Synthetic 003 mRNA.				
ACCESSION	M22020				
VERSION	M22020.1 GI:208873				
KEYWORDS	artificial gene.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 111)				
AUTHORS	Calogero,R.A., Pon,C.L., Canonaco,M.A. and Gualerzi,C.O.				
TITLE	Selection of the mRNA translation initiation region by Escherichia coli ribosomes				
JOURNAL	Proc.Natl. Acad. Sci. U.S.A. 85 (17), 6427-6431 (1988)				
MEDLINE	88320453				
PUBMED	3045816				
COMMENT	Original source text: Synthetic mRNA, clone pXR003.				
FEATURES	Location/Qualifiers				
source	1..111				
	/organism="synthetic construct"				
	/mol_type="mRNA"				
	/db_xref="taxon:32630"				
	1..111				
	/product="003 mRNA"				
	25..57				
	/note="003 mRNA peptide"				
	/codon_start=1				

/transl_table=11 /protein_id="AAA72693.1" /db_xref="GI:208874" /translation="MFTITTIFFT"									
ORIGIN									
Alignment Scores:									
Pred. No.:	253	Length:	111						
Score:	27.00	Matches:	6						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	100.00%	Indels:	0						
DB:	12	Gaps:	0						
US-10-014-101B-41 (1-6) x SYNMRNA03 (1-111)									
QY	1 IleThrArgAlaArgile 6								
Db	21 ATAACAAGGGCCCGAATT 4								
RESULT 2									
BV079618	BV079618 130 bp DNA linear STS 20-JUL-2004								
LOCUS	E2M2-130 Hessian fly genomic DNA Mayetiola destructor STS genomic, sequence tagged site.								
DEFINITION									
ACCESSION	BV079618								
VERSION	BV079618.1 GI:34787367								
KEYWORDS	STS.								
SOURCE	Mayetiola destructor (Hessian fly)								
ORGANISM	Mayetiola destructor								
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea; Cecidomyiidae; Mayetiola.								
REFERENCE	1 (bases 1 to 130)								
AUTHORS	Behura,S.K., Valicente,F.H., Rider,S.D. Jr., Shun-Chen,M., Jackson,S. and Stuart,J.J.								
TITLE	A physically anchored genetic map and linkage to avirulence reveals recombination suppression over the proximal region of hessian fly chromosome A2								
JOURNAL	Genetics 167 (1), 343-355 (2004)								
PUBMED	15166159								
COMMENT	Contact: Jeff Stuart Department of Entomology Purdue University 901 W State St., West Lafayette, IN 47907, USA Primer A: None provided Primer B: None provided Protocol: Template: 20-30ng Primer: each 20 pmoles dNTPs: each 2000uM Taq Pol: 0.1 units/ul Total Vol: 25 ul								
Buffer:									
	MgCl2:	2.5mM							
	KCl:	50 mM							
	Tris-Cl:	10mM							
	pH:	8.3.							
Location/Qualifiers									
1..130									
/organism="Mayetiola destructor"									
/mol_type="genomic DNA"									
/db_xref="taxon:39758"									
/clone_lib="Hessian fly genomic DNA"									
<1..>130									
STS									
ORIGIN									
Alignment Scores:									
Pred. No.:	294	Length:	130						
Score:	27.00	Matches:	6						
Percent Similarity:	100.00%	Conservative:	0						

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0
US-10-014-101B-41 (1-6) x BV079618 (1-130)			
QY	1 IleThrArgAlaArgile 6		
Db	36 ATAACCAGGGCTAGAATA 53		
RESULT 3			
HVU234763	HVU234763 151 bp DNA linear PLN 07-JAN-2000		
LOCUS	Hordeum vulgare genomic DNA fragment; clone MWG2081.rev.		
DEFINITION			
ACCESSION	AJ234763		
VERSION	AJ234763.1 GI:3819546		
KEYWORDS	RFLP marker.		
SOURCE	Hordeum vulgare subsp. vulgare		
ORGANISM	Hordeum vulgare subsp. vulgare		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.		
REFERENCE	1 (bases 1 to 151)		
AUTHORS	Michalek,W., Kunzel,G. and Graner,A.		
TITLE	Sequence analysis and gene identification in a set of mapped RFLP markers in barley (Hordeum vulgare)		
JOURNAL	Genome 42 (5), 849-853 (1999)		
MEDLINE	20051696		
PUBMED	10584307		
REFERENCE	2 (bases 1 to 151)		
AUTHORS	Michalek,W.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-OCT-1998) Michalek W., Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466 Gatersleben, Germany		
FEATURES			
source		Location/Qualifiers	
1..151			
/organism="Hordeum vulgare subsp. vulgare"			
/mol_type="genomic DNA"			
/cultivar="Igr1"			
/sub_species="vulgare"			
/db_xref="taxon:112509"			
/clone="MWG2081.rev"			
/tissue_type="leaf"			
misc_feature		1..151	
/note="vector: pBluescript; Primer: M13rev"			
ORIGIN			
Alignment Scores:		Length: 151	
Pred. No.:	340	Matches:	6
Score:	27.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	8		
US-10-014-101B-41 (1-6) x HVU234763 (1-151)			
QY	1 IleThrArgAlaArgile 6		
Db	87 ATCACCAGGGCAAGAATT 104		
RESULT 4			
AX935409	AX935409 159 bp DNA linear PAT 05-JAN-2004		
LOCUS	Sequence 13 from Patent WO03089475.		
DEFINITION			
ACCESSION	AX935409		
VERSION	AX935409.1 GI:40642182		
KEYWORDS			
SOURCE	Raphanus sativus (radish)		
ORGANISM	Raphanus sativus		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		

rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

REFERENCE 1
AUTHORS Peschen,D., Fischer,R., Schillberg,S., Liao,Y.C. and Dorfmueller,S.
TITLE Antibodies, recombinant antibodies, recombinant antibody fragments
and fusions mediated plant disease resistance against fungi
JOURNAL Patent: WO 03089475-A 13 30-OCT-2003;
Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung
e.V. (DE)

FEATURES
source Location/Qualifiers
1. .159
/organism="Raphanus sativus"
/mol_type="unassigned DNA"
/db_xref="taxon:3726"

ORIGIN

Alignment Scores:
Pred. No.: 357 Length: 159
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x AX935409 (1-159)

Qy 1 IleThrArgAlaArgIle 6
Db 59 ATAACGCGTGAAGAATC 76

RESULT 5
CQ648448/c
LOCUS CQ648448 192 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5405 from Patent WO0234771.
ACCESSION CQ648448
VERSION CQ648448.1 GI:41683950
KEYWORDS
SOURCE Streptococcus agalactiae
ORGANISM Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

REFERENCE 1
AUTHORS Telford,J., Masignani,V., Margarit y Ros,I., Grandi,G., Fraser,C.
and Tettelin,H.
TITLE Nucleic acids and proteins from streptococcus groups a & b
JOURNAL Patent: WO 0234771-A 5405 02-MAY-2002;
Chiron S.p.A. (IT) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)

FEATURES
source Location/Qualifiers
1. .192
/organism="Streptococcus agalactiae"
/mol_type="unassigned DNA"
/db_xref="taxon:1311"

ORIGIN

Alignment Scores:
Pred. No.: 429 Length: 192
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CQ648448 (1-192)

Qy 1 IleThrArgAlaArgIle 6
Db 116 ATAACAAGAGCAAGAATT 99

RESULT 6
CQ651934/c
LOCUS CQ651934 195 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8891 from Patent WO0234771.
ACCESSION CQ651934
VERSION CQ651934.1 GI:41685756

KEYWORDS Streptococcus agalactiae

SOURCE Streptococcus agalactiae

ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

REFERENCE 1

AUTHORS Telford,J., Masignani,V., Margarit y Ros,I., Grandi,G., Fraser,C.
and Tettelin,H.
TITLE Nucleic acids and proteins from streptococcus groups a & b
JOURNAL Patent: WO 0234771-A 8891 02-MAY-2002;
Chiron S.p.A. (IT) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)

FEATURES
source Location/Qualifiers
1. .195
/organism="Streptococcus agalactiae"
/mol_type="unassigned DNA"
/db_xref="taxon:1311"

ORIGIN

Alignment Scores:
Pred. No.: 435 Length: 195
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CQ651934 (1-195)

Qy 1 IleThrArgAlaArgIle 6
Db 116 ATAACAAGAGCAAGAATT 99

RESULT 7
AX607583/c
LOCUS AX607583 195 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 5512 from Patent WO02092818.
ACCESSION AX607583
VERSION AX607583.1 GI:28403115
KEYWORDS
SOURCE Streptococcus agalactiae
ORGANISM Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

REFERENCE 1

AUTHORS Glaser,P., Rusniok,C., Chevalier,F., Frangeul,L., Lalioui,L.,
Zouine,M., Couve,E., Buchrieser,C., Poyart,C., Trieu-Cuot,P. and
Kunst,F.
TITLE Streptococcus agalactiae genome sequence, use for developing
vaccines, diagnostic tools, and for identifying therapeutic targets
JOURNAL Patent: WO 02092818-A 5512 21-NOV-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES
source Location/Qualifiers
1. .195
/organism="Streptococcus agalactiae"
/mol_type="unassigned DNA"
/db_xref="taxon:1311"

ORIGIN

Alignment Scores:
Pred. No.: 435 Length: 195
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x AX607583 (1-195)

Qy 1 IleThrArgAlaArgIle 6
Db 116 ATAACAAGAGCAAGAATT 99


```
RESULT 8
AF490285/c
LOCUS      AF490285              372 bp    DNA        linear    PLN 26-JUL-2002
DEFINITION Phytophthora mirabilis strain 3010 clone 1 gypsy-like
            retrotransposon, partial sequence.
ACCESSION  AF490285
VERSION     AF490285.1  GI:20386310
KEYWORDS
SOURCE      Phytophthora mirabilis
ORGANISM    Phytophthora mirabilis
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 372)
AUTHORS    Judelson,H.S.
TITLE      Sequence Variation and Genomic Amplification of a Family of
            Gypsy-like Elements in the Oomycete Genus Phytophthora
JOURNAL    Mol. Biol. Evol. 19 (8), 1313-1322 (2002)
MEDLINE    22135996
PUBMED     12140243
REFERENCE   2  (bases 1 to 372)
AUTHORS    Judelson,H.S.
TITLE      Direct Submission
JOURNAL    Submitted (01-MAR-2002) Dept. of Plant Pathology, University of
            California, Webber Hall, Riverside, CA 92521, USA
            Contains probable non-functional element.
COMMENT
FEATURES
            source
                1..372
                /organism="Phytophthora mirabilis"
                /mol_type="genomic DNA"
                /strain="3010"
                /db_xref="taxon:129356"
                /clone="1"
            repeat_region
                <1..>372
                /transposon="gypsy-like retrotransposon"
ORIGIN
Alignment Scores:
Pred. No.:      812          Length:      372
Score:          27.00       Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             8           Gaps:        0

US-10-014-101B-41 (1-6) x AF490285 (1-372)

Qy      1  lleThrArgAlaArgile 6
        |||||||
Db      206 ATTACGGGGCAAGAATC 189

RESULT 9
AF490286/c
LOCUS      AF490286              372 bp    DNA        linear    PLN 26-JUL-2002.
DEFINITION Phytophthora mirabilis strain 3010 clone 2 gypsy-like
            retrotransposon, partial sequence.
ACCESSION  AF490286
VERSION     AF490286.1  GI:20386311
KEYWORDS
SOURCE      Phytophthora mirabilis
ORGANISM    Phytophthora mirabilis
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 372)
AUTHORS    Judelson,H.S.
TITLE      Sequence Variation and Genomic Amplification of a Family of
            Gypsy-like Elements in the Oomycete Genus Phytophthora
JOURNAL    Mol. Biol. Evol. 19 (8), 1313-1322 (2002)
MEDLINE    22135996
PUBMED     12140243
REFERENCE   2  (bases 1 to 372)
AUTHORS    Judelson,H.S.
TITLE      Direct Submission
JOURNAL    Submitted (01-MAR-2002) Dept. of Plant Pathology, University of
```

```
California, Webber Hall, Riverside, CA 92521, USA
            Contains probable non-functional element.
COMMENT
FEATURES
            source
                1..372
                /organism="Phytophthora mirabilis"
                /mol_type="genomic DNA"
                /strain="3010"
                /db_xref="taxon:129356"
                /clone="2"
            repeat_region
                <1..>372
                /transposon="gypsy-like retrotransposon"
ORIGIN
Alignment Scores:
Pred. No.:      812          Length:      372
Score:          27.00       Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             8           Gaps:        0

US-10-014-101B-41 (1-6) x AF490286 (1-372)

Qy      1  lleThrArgAlaArgile 6
        |||||||
Db      206 ATTACGGGGCAAGAATC 189

RESULT 10
AF408671/c
LOCUS      AF408671              393 bp    DNA        linear    INV 18-FEB-2002
DEFINITION Trichogramma alpha strain ACLE internal transcribed spacer 2,
            complete sequence.
ACCESSION  AF408671
VERSION     AF408671.1  GI:18699085
KEYWORDS
SOURCE      Trichogramma alpha
ORGANISM    Trichogramma alpha
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
            Trichogrammatidae; Trichogramma.
REFERENCE   1  (bases 1 to 393)
AUTHORS    Pinto,J.D., Koopmanschap,A.B., Platner,G.R. and Stouthamer,R.
TITLE      The North American Trichogramma (Hymenoptera: Trichogrammatidae)
            parasitizing certain Tortricidae (Lepidoptera) on apple and pear,
            with ITS2 DNA characterizations and description of a new species
JOURNAL    Biol. Control 23, 134-142 (2002)
REFERENCE   2  (bases 1 to 393)
AUTHORS    Pinto,J.D., Koopmanschap,A.B., Platner,G.R. and Stouthamer,R.
TITLE      Direct Submission
JOURNAL    Submitted (10-AUG-2001) Entomology, University of California,
            Riverside, CA 92521, USA
FEATURES
            source
                1..393
                /organism="Trichogramma alpha"
                /mol_type="genomic DNA"
                /strain="ACLE"
                /db_xref="taxon:185869"
                1..393
                /product="internal transcribed spacer 2"
            misc_rna
ORIGIN
Alignment Scores:
Pred. No.:      857          Length:      393
Score:          27.00       Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             3           Gaps:        0

US-10-014-101B-41 (1-6) x AF408671 (1-393)

Qy      1  lleThrArgAlaArgile 6
        |||||||
```

Db 334 ATAACGGCGCGCGCATT 317

RESULT 11
AF408673/c
LOCUS
DEFINITION Trichogramma alpha strain ADRK internal transcribed spacer 2,
complete sequence.
ACCESSION AF408673
VERSION AF408673.1 GI:18699087
KEYWORDS
SOURCE Trichogramma alpha
ORGANISM Trichogramma alpha
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
Trichogrammatidae; Trichogramma.
REFERENCE 1 (bases 1 to 395)
AUTHORS Pinto,J.D., Koopmanschap,A.B., Platner,G.R. and Stouthamer,R.
TITLE The North American Trichogramma (Hymenoptera: Trichogrammatidae)
parasitizing certain Tortricidae (Lepidoptera) on apple and pear,
with ITS2 DNA characterizations and description of a new species
JOURNAL Biol. Control 23, 134-142 (2002)
REFERENCE 2 (bases 1 to 395)
AUTHORS Pinto,J.D., Koopmanschap,A.B., Platner,G.R. and Stouthamer,R.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2001) Entomology, University of California,
Riverside, CA 92521, USA

FEATURES
source Location/Qualifiers
1..395
/organism="Trichogramma alpha"
/mol_type="genomic DNA"
/strain="ADRK"
/db_xref="taxon:185869"
1..395
/product="internal transcribed spacer 2"

misc_RNA

ORIGIN
Alignment Scores: Length: 395
Pred. No.: 861 Matches: 6
Score: 27.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AF408673 (1-395)

QY 1 IleThrArgAlaArgIle 6
|||||

Db 336 ATAACGGCGCGCGCATT 319

RESULT 12
AF408672/c
LOCUS
DEFINITION Trichogramma alpha strain ACOL internal transcribed spacer 2,
complete sequence.
ACCESSION AF408672
VERSION AF408672.1 GI:18699086
KEYWORDS
SOURCE Trichogramma alpha
ORGANISM Trichogramma alpha
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
Trichogrammatidae; Trichogramma.
REFERENCE 1 (bases 1 to 397)
AUTHORS Pinto,J.D., Koopmanschap,A.B., Platner,G.R. and Stouthamer,R.
TITLE The North American Trichogramma (Hymenoptera: Trichogrammatidae)
parasitizing certain Tortricidae (Lepidoptera) on apple and pear,
with ITS2 DNA characterizations and description of a new species
JOURNAL Biol. Control 23, 134-142 (2002)
REFERENCE 2 (bases 1 to 397)
AUTHORS Pinto,J.D., Koopmanschap,A.B., Platner,G.R. and Stouthamer,R.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2001) Entomology, University of California,

Riverside, CA 92521, USA

FEATURES
source Location/Qualifiers
1..397
/organism="Trichogramma alpha"
/mol_type="genomic DNA"
/strain="ACOL"
/db_xref="taxon:185869"
1..397
/product="internal transcribed spacer 2"

misc_RNA

ORIGIN
Alignment Scores: Length: 397
Pred. No.: 865 Matches: 6
Score: 27.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AF408672 (1-397)

QY 1 IleThrArgAlaArgIle 6
|||||

Db 334 ATAACGGCGCGCGCATT 317

RESULT 13
G58417/c
LOCUS
DEFINITION SHGC-104567 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G58417
VERSION G58417.1 GI:6123736
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT
Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School Of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TGAATCTGATGGGCTCAATAAAA
Primer B: CCTGGTTGGATGGAACCTATT
STS size: 322
PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
AmpliTaq Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul
Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

BAC ends sequenced at TIGR from the RPC111 BAC library. Designed and developed at the Stanford Human Genome Center.


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intron      <1..514
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trNA        <515..>546
            /gene="trnL"
            /product="tRNA-Leu"

ORIGIN
Alignment Scores:
Pred. No.:      1.18e+03      Length:      546
Score:          27.00         Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              8           Gaps:          0

US-10-014-101B-41 (1-6) x AY191142 (1-546)

Qy      1 IleThrArgAlaArgile 6
Db      449 ATTACTCGGCGAGAATA 466

RESULT 17
AY191137
LOCUS
DEFINITION
Pyricularia sinensis tRNA-Leu (trnL) gene, partial sequence;
chloroplast gene for chloroplast product.
ACCESSION
AY191137
VERSION
AY191137.1 GI:37779722
KEYWORDS
SOURCE
ORGANISM
Pyricularia sinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Pyricularia.
REFERENCE
1 (bases 1 to 547)
AUTHORS
Han,R.L., Hao,G. and Zhang,D.X.
TITLE
Interfamilial relationships as revealed by chloroplast trnL intron
sequences
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 547)
AUTHORS
Han,R.L., Hao,G. and Zhang,D.X.
TITLE
Direct Submission
JOURNAL
Submitted (05-DEC-2002) Centre for Systematic and Evolutionary
Botany, South China Institute of Botany, Leyiju, Guangzhou,
Guangdong 510650, P.R. China
FEATURES
source
1..547
Location/Qualifiers
/organism="Pyricularia sinensis"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
/db_xref="taxon:227912"
<1..>547
/gene="trnL"
<1..531
/gene="trnL"
<532..>547
/gene="trnL"
/product="tRNA-Leu"

gene
intron
trNA

ORIGIN
Alignment Scores:
Pred. No.:      1.18e+03      Length:      547
Score:          27.00         Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              8           Gaps:          0

US-10-014-101B-41 (1-6) x AY191137 (1-547)

Qy      1 IleThrArgAlaArgile 6
Db      456 ATTACTCGGCGAGAATA 473
```

```
RESULT 18
AF096559
LOCUS
DEFINITION
Rattus norvegicus clone D5Uwm49, sequence tagged site.
ACCESSION
AF096559
VERSION
AF096559.1 GI:5565747
KEYWORDS
STS.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 555)
Lan,H., Shepel,L.A., Haag,J.D. and Gould,M.N.
Linkage mapping of rat chromosome 5 markers generated from
chromosome-specific libraries
Mamm. Genome 10 (7), 687-691 (1999)
99315326
10384040
2 (bases 1 to 555)
Lan,H., Shepel,L.A., Haag,J.D. and Gould,M.N.
Direct Submission
Submitted (02-OCT-1998) McArdle Laboratory for Cancer Research,
University of Wisconsin Medical School, 1400 University Avenue,
Madison, WI 53706, USA
FEATURES
source
1..555
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Copenhagen"
/db_xref="taxon:10116"
/chromosome="5"
/clone="D5Uwm49"
215..235
primer_bind
complement(446..463)
primer_bind
ORIGIN
Alignment Scores:
Pred. No.:      1.2e+03      Length:      555
Score:          27.00         Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              11         Gaps:          0

US-10-014-101B-41 (1-6) x AF096559 (1-555)

Qy      1 IleThrArgAlaArgile 6
Db      78 ATAAC TAGAGCTAGGATT 95

RESULT 19
BV192133/c
LOCUS
DEFINITION
sgnm173469 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION
BV192133
VERSION
BV192133.1 GI:48034424
KEYWORDS
STS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 601)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press
JOURNAL
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
```


Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 601.

FEATURES

source
1..601
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
<1..>601

STS

ORIGIN

Alignment Scores:
Pred. No.: 1.29e+03 Length: 601
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-41 (1-6) x BV192133 (1-601)

QY 1 IleThrArgAlaArgile 6

Db 482 ATAAGCTAGGCTAGGATT 465

RESULT 20

AF232017/c

LOCUS

DEFINITION Tamandua tetradactyla clone 1 cytochrome b gene, partial cds, mitochondrial gene for mitochondrial product.

ACCESSION AF232017

VERSION AF232017.1 GI:13128889

KEYWORDS

SOURCE

ORGANISM

mitochondrion Tamandua tetradactyla (southern tamandua)

Tamandua tetradactyla

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Edentata; Myrmecophagidae; Tamandua.

1 (bases 1 to 648)

Greenwood,A.D., Castresana,J., Feldmaier-Fuchs,G. and Paabo,S.

A molecular phylogeny of two extinct sloths

Mol. Phylogenet. Evol. 18 (1), 94-103 (2001)

21097350

PUBMED

2 (bases 1 to 648)

Greenwood,A.D., Castresana,J., Feldmaier-Fuchs,G. and Paabo,S.

Direct Submission

Submitted (08-FEB-2000) Vertebrate Zoology, American Museum of

Natural History, Central Park West at 79th Street, New York, NY

10024, USA

FEATURES

source

Location/Qualifiers

1..648

/organism="Tamandua tetradactyla"

/organelle="mitochondrion"

/mol_type="genomic DNA"

/db_xref="taxon:48850"

/clone="1"

1..>648

/codon_start=1

/transl_table=2

/product="cytochrome b"

/protein_id="AAK13065.1"

/db_xref="GI:13128890"

/translation="MTHIRKTHPLFKIINQSFIDLPAPSNISAWNFGSLGLCLIIQ

ILTGLFLAMHYTSDTITAFSSVTHICRDVNYGWLRIYIHASGASFMCLYLHYVGRGL

YVGSFLYLETWNIGVILLATMATTFMGVLPWGQMSFWGATVITNLLSAIPYIGTDL

VEWIGGFSVDKATLTRFFAFHFILPFIIALVMTHLLFLHETGSNNPLGLSSAMD"

ORIGIN

Alignment Scores:

Pred. No.: 1.39e+03 Length: 648
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x AF232017 (1-648)

QY 1 IleThrArgAlaArgile 6

Db 581 ATTACTAGGCTAGGATA 564

RESULT 21

AY330210

LOCUS

DEFINITION Toxoplasma gondii clone TgSat350-3 satellite DNA sequence.

ACCESSION AY330210

VERSION AY330210.1 GI:33243869

KEYWORDS

SOURCE

ORGANISM

Toxoplasma gondii

Toxoplasma gondii

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Toxoplasma.

1 (bases 1 to 700)

Clemente,M., De Miguel,N., Lia,V.V., Matrajt,M. and Angel,S.O.

Structure Analysis of Two Toxoplasma gondii and Neospora caninum

Satellite DNA Families and Evolution of Their Common Monomeric

Sequence

J. Mol. Evol. 58 (5), 557-567 (2004)

PUBMED

2 (bases 1 to 700)

Clemente,M., de Miguel,N. and Angel,S.O.

Direct Submission

Submitted (24-JUN-2003) Parasitologia Molecular, IIB-INTECH, Camino

de Circunvalacion Laguna Km 6, Chascomus, Buenos Aires B7130IIWA,

Argentina

Location/Qualifiers

1..700

/organism="Toxoplasma gondii"

/mol_type="genomic DNA"

/db_xref="taxon:5811"

/clone="TgSat350-3"

repeat_region 1..700

/note="satellite"

ORIGIN

Alignment Scores:

Pred. No.: 1.5e+03 Length: 700
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AY330210 (1-700)

QY 1 IleThrArgAlaArgile 6

Db 428 ATCACTCGGGCAGCAATT 445

RESULT 22

HSA327616

LOCUS

DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone

HSA327616

NR1-CF6R.

AJ327616

VERSION AJ327616.1 GI:15872034

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitski,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
Noti flanking sequences: a tool for gene discovery and verification of the human genome

Nucleic Acids Res. 30 (14), 3163-3170 (2002)
22131767

12136098
2 (bases 1 to 724)
Zabarovsky,E.R.

Direct Submission
Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

Location/Qualifiers
1. .724
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NR1-CF6R"

ORIGIN

Alignment Scores:
Pred. No.: 1.55e+03 Length: 724
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-41 (1-6) x HSA327616 (1-724)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 172 ATTACCCGGCAGGTATA 189

RESULT 23
AY330204
LOCUS Neospora caninum clone Ncsat350-2 DNA linear INV 07-JUN-2004
DEFINITION Neospora caninum clone Ncsat350-2 satellite DNA sequence.
ACCESSION AY330204
VERSION AY330204.1 GI:33243692
KEYWORDS
SOURCE Neospora caninum
ORGANISM Neospora caninum

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Neospora.
1 (bases 1 to 730)
Clemente,M., De Miguel,N., Lia,V.V., Matrajt,M. and Angel,S.O.
Structure Analysis of Two Toxoplasma gondii and Neospora caninum Satellite DNA Families and Evolution of Their Common Monomeric Sequence

J. Mol. Evol. 58 (5), 557-567 (2004)
15170259
2 (bases 1 to 730)
Clemente,M., de Miguel,N. and Angel,S.O.
Direct Submission
Submitted (23-JUN-2003) Parasitologia Molecular, IIB-INTECH, Camino de Circunvalacion Laguna Km 6, Chascomus, Buenos Aires B7130IWA, Argentina

Location/Qualifiers
1. .730
/organism="Neospora caninum"
/mol_type="genomic DNA"
/db_xref="taxon:29176"
/clone="Ncsat350-2"
repeat_region 1. .730
/note="satellite"

ORIGIN

Alignment Scores:
Pred. No.: 1.56e+03 Length: 730
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AY330204 (1-730)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 458 ATCACTCGGCACGAATT 475

RESULT 24
AJ606422/c
LOCUS Marmosops impavidus mitochondrial partial cyt-b gene for cytochrome
DEFINITION b.
AJ606422 800 bp mRNA linear MAM 17-MAY-2004
Marmosops impavidus mitochondrial partial cyt-b gene for cytochrome

ACCESSION AJ606422
VERSION AJ606422.1 GI:47457369
KEYWORDS cyt-b gene; cytochrome b.
SOURCE Mitochondrion Marmosops impavidus (Andean slender mouse opossum)
ORGANISM Marmosops impavidus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
1
Steiner,C.C. and Catzefflis,F.M.
Genetic variation and geographical structure of five mouse-sized opossums (Marsupialia, Didelphidae) throughout the Guiana Region
J. Biogeogr. 31 (6), 959-973 (2004)
REFERENCE 2 (bases 1 to 800)
AUTHORS Steiner,C.C.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2003) Steiner C.C., Institut des Sciences de l'Evolution, Universite Montpellier II, Place Eugene Bataillon CC064, Montpellier 34095 cedex 05, FRANCE

Location/Qualifiers
1. .800
/organism="Marmosops impavidus"
/organelle="mitochondrion"
/mol_type="mRNA"
/db_xref="taxon:42722"
/tissue_type="liver"
/country="Peru:Loreto, Rio Galvez"
1. .800
/gene="cyt-b"
1. .>800
/gene="cyt-b"
/codon_start=1
/transl_table=2
/product="cytochrome b"
/protein_id="CAE54498.1"
/db_xref="GI:47457370"

translation="MTNLRKTHPLIKIINHSTFDLPAPSNISAWNFGSLGICLI IQ
ILTGLFLAMHYTSDTLTAFSSVAHICRDVNYGLRNHLHANGASMFMCFLHVGRI
YGYSMFKETWNIGVILLTVMATAFVGYYLPGQMSFWGATVITNLLSAIPYIGTTL
VEWINGGFSVDKATLTFRFAHFILPFIILALVHLLFLHETGSNNPTGINPDSDKI
PFHPYYTIKDALGLILMITLLSLALFSPDMLGDPDNFTPANPLNTPP"

ORIGIN

Alignment Scores:
Pred. No.: 1.7e+03 Length: 800
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x AJ606422 (1-800)

Qy 1 IleThrArgAlaArgile 6

Db 581 ATTACTAGGCTAGGATA 564

RESULT 25
AF534679

LOCUS AF534679 805 bp DNA linear PLN 02-SEP-2003
DEFINITION Pyricularia edulis chloroplast trnA-Leu (trnL) gene, partial sequence and trnL-trnF intergenic spacer region.
ACCESSION AF534679
VERSION AF534679.1 GI:33330318
KEYWORDS
SOURCE chloroplast Pyricularia edulis
ORGANISM Pyricularia edulis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae; Pyricularia.
REFERENCE 1 (bases 1 to 805)
AUTHORS Yang,S.-X., Yang,J.-B., Peng,H. and Li,D.-Z.
TITLE The systematic relationship of Pentaphragylacaceae: inference from trnL-F (cpDNA) sequence data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 805)
AUTHORS Yang,S.-X., Yang,J.-B., Peng,H. and Li,D.-Z.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-2002) Plant Taxonomy and Phytogeography, Kunming Institute of Botany, Heilongtan, Kunming, Yunnan 650204, P.R. China

FEATURES
source 1..805
/organism="Pyricularia edulis"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
/db_xref="taxon:212710"
misc_feature <1..>805
/note="contains trnA-Leu (trnL) gene and trnL-trnF intergenic spacer region"

ORIGIN

Alignment Scores:
Pred. No.: 1.71e+03 Length: 805
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x AF534679 (1-805)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 430 ATTACTCGGCGAGAATA 447

RESULT 26
ZMU82201

LOCUS ZMU82201 816 bp mRNA linear PLN 06-JUL-1998
DEFINITION Zea mays pathogenesis related protein-5 (PR-5) mRNA, complete cds.
ACCESSION U82201
VERSION U82201.1 GI:3290005
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 816)
AUTHORS Morris,S.W., Vernooij,B., Titatarn,S., Starrett,M., Thomas,S., Wiltse,C.C., Frederiksen,R.A., Bhandhufalck,A., Hulbert,S. and Uknes,S.
TITLE Induced resistance responses in maize
JOURNAL Mol. Plant Microbe Interact. 11 (7), 643-658 (1998)
MEDLINE 98313983
PUBMED 9650297
REFERENCE 2 (bases 1 to 816)
AUTHORS Morris,S.W., Vernooij,B., Hulbert,S., Starrett,M., Thomas,S. and

Uknes,S.
Direct Submission
Submitted (13-DEC-1996) Ciba-Geigy, P.O. Box 12257, Research Triangle Park, NC 27709-2257, USA
FEATURES
source 1..816
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
gene 1..816
/gene="PR-5"
CDS 63..581
/gene="PR-5"
/codon_start=1
/product="pathogenesis related protein-5"
/protein_id="AAC25630.1"
/db_xref="GI:3290006"
/translation="MAAASSVLLLLLLAALAGMSANAATFTTNCGFTVWPAATPVG GGTQLNPGGTWTVNPAGTSSGRVWGRTGCSFNGNSGSCQTGDCGGALACTLSGQPPL TLAFTTIGSQDFYDISVIDGYNLAMAFSCSTGVRLVCTDPGCPDAYHNPDPDMKTHAC GGNSNYQVTFCP"

ORIGIN

Alignment Scores:
Pred. No.: 1.74e+03 Length: 816
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x ZMU82201 (1-816)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 675 ATTACACGTGCACGCATT 692

RESULT 27
BV065128/c

LOCUS BV065128 860 bp DNA linear STS 31-MAY-2003
DEFINITION S212P60513FE11.T0 CZECHII/Ei Mus musculus STS genomic, sequence tagged site.
ACCESSION BV065128
VERSION BV065128.1 GI:31180923
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 860)
AUTHORS Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C., Lander,E.S., Lindblad-Toh,K. and Daly,M.J.
TITLE The mosaic structure of variation in the laboratory mouse genome
JOURNAL Nature 420 (6915), 574-578 (2002)
MEDLINE 22354684
PUBMED 12466852
COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 860
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated

as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

FEATURES

source
1. .860
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map=" + 2 28-808 147970603-147971383"
/clone_lib="CZECHII/Ei"
<1. .>860

STS

ORIGIN

Alignment Scores:
Pred. No.: 1.83e+03 Length: 860
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-41 (1-6) x BV065128 (1-860)

Qy 1 IletHrArgAlaArgile 6

Db 43 ATCACAAGAGCCAGAATA 26

RESULT 28

AK1033395

LOCUS

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J033127M23, full insert sequence.

ACCESSION

AK1033395

VERSION

AK103395.1 GI:32988604

KEYWORDS

FLI_CDNA; CAP trapper.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1
The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ootomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

TITLE

JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764

REFERENCE

AUTHORS

2 (bases 1 to 872)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

Direct Submission

TITLE

JOURNAL

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression: 2-1-2 Kannondai, Tsukuba, Ibaraki

305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,

Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica

rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/

NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,

Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,

Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and

Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,

Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,

Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,

Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,

Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,

Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center

and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,

Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,

Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,

Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,

Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,

Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,

Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,

Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,

Yasunishi,A. and Hayashizaki,Y.

FEATURES

source

1. .872
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033127M23"

ORIGIN

Alignment Scores:
Pred. No.: 1.85e+03 Length: 872
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x AK103395 (1-872)

Qy 1 IletHrArgAlaArgile 6

Db 206 ATTACGCGCGCAAGATC 223

RESULT 29

BD275463

LOCUS

BD275463

874 bp

DNA

linear

PAT 17-JUL-2003

DEFINITION 47 Human Secreted Proteins.
ACCESSION BD275463
VERSION BD275463.1 GI:33085231
KEYWORDS JP 2002539831-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Rosen,C.A., Ruben,S.M. and Komatsoulis,G.
TITLE 47 Human Secreted Proteins
JOURNAL Patent: JP 2002539831-A 21 26-NOV-2002;
COMMENT Human Genome Sciences Inc
OS Homo sapiens
PN JP 2002539831-A/21
PD 26-NOV-2002
PF 22-MAR-2000 JP 2000608749
PR 22-DEC-1999 US 60/171550,26-MAR-1999 US 60/126600 PI
craig a rosen,steven m ruben,george komatsoulis CC
FH Key Location/Qualifiers.
FEATURES
source 1. .874
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores: 1.85e+03 Length: 874
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6
US-10-014-101B-41 (1-6) x BD275463 (1-874)
QY 1 IleThrArgAlaArgIle 6
Db 717 ATAACAAGGGCTAGAATA 734
RESULT 30
CNS06ELJ 887 bp DNA linear STS 10-JAN-2001
LOCUS T7 end of clone AR0AA022E09 of library AR0AA from strain CBS 732 of
DEFINITION Zygosaccharomyces rouxii, sequence tagged site.
ACCESSION AL395261
VERSION AL395261.1 GI:12146730
KEYWORDS STS.
SOURCE Zygosaccharomyces rouxii
ORGANISM Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Zygosaccharomycetaceae; Zygosaccharomyces.
REFERENCE 1 (bases 1 to 887)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 887)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekaia,F., Dujon,B., Wincker,P., Artiguenave,F. and Souciet,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
JOURNAL Zygosaccharomyces rouxii
MEDLINE 20584718
PUBMED 11152883

REFERENCE 3 (bases 1 to 887)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES
source Location/Qualifiers
1. .887
/organism="Zygosaccharomyces rouxii"
/mol_type="genomic DNA"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0AA022E09"
/clone_lib="AR0AA"
/note="end : T7"
misc_feature <3..>407
/note="similar to Saccharomyces cerevisiae ORF YPR173c [VPS4 ; vacuolar sorting protein]"
misc_feature complement(<539..>886)
/note="similar to Saccharomyces cerevisiae ORF YLR456w [strong similarity to YPR172w]"
misc_feature complement(<548..>886)
/note="similar to Saccharomyces cerevisiae ORF YPR172w [strong similarity to YLR456w]"
ORIGIN
Alignment Scores: 1.88e+03 Length: 887
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 11
US-10-014-101B-41 (1-6) x CNS06ELJ (1-887)
QY 1 IleThrArgAlaArgIle 6
Db 281 ATTACAAGAGCCAGAATT 298
RESULT 31
E16279 900 bp DNA linear PAT 28-JUL-1999
LOCUS gDNA encoding ubiquitin.
DEFINITION E16279
ACCESSION E16279
VERSION E16279.1 GI:5710962
KEYWORDS JP 1998150989-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 900)
AUTHORS Tomota,A. and Koike,M.
TITLE UBIQUITIN GENE
JOURNAL Patent: JP 1998150989-A 1 09-JUN-1998;
COMMENT NOYAKU BIO TECHNOL KAIHATSU GIJUTSU KENKYU KUMIAI
OS Maestra brassicae nuclear polyhedrosis virus PN 1998150989-A/1
PD 09-JUN-1998
PF 26-NOV-1996 JP 1996315069
PI TOMOTA AKIHIRO, KOIKE MASARU

PC C12N15/09,C07H21/04//C07K14/01,(C12N15/09,C12R1:92); CC
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
FT source 1..900
FT /organism='Mamestra brassicae nuclear FT
FT polyhedrosis virus'
FT 5'UTR 1..405
FT CDS 406..708
FT /product='Ubiquitin'
FT 3'UTR 709..900.
FEATURES
source
1..900
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 1..91e+03 Length: 900
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x B16279 (1-900)

QY 1 IleThrArgAlaArgile 6
|||||
Db 656 ATAACCCGGGCTCGAATA 673

RESULT 32
AF434177/c

LOCUS AF434177 984 bp DNA linear MAM 17-OCT-2002
DEFINITION Thylamys elegans isolate NK 95622 cytochrome b (cyt b) gene,
partial cds; mitochondrial gene for mitochondrial product.
ACCESSION AF434177
VERSION AF434177.1 GI:24078500
KEYWORDS
SOURCE
ORGANISM
Thylamys elegans
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Thylamys.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 984)
Meynard,A.P., Palma,R.E. and Rivera-Milla,E.
Filogeografia de las llacas chilenas del genero Thylamys
(Marsupialia, Didelphidae) en base a secuencias del gen
mitochondrial citocromo b
Rev. Chil. Hist. Nat. (2002) In press
REFERENCE
AUTHORS
TITLE
2 (bases 1 to 984)
Meynard,A.P., Palma,R.E. and Rivera-Milla,E.
Direct Submission
Submitted (16-OCT-2001) Ecologia, P. Universidad Catolica de Chile,
Casilla 114-D, Santiago, Santiago 6513677, Chile
FEATURES
source
1..984
/organism="Thylamys elegans"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="NK 95622"
/db_xref="taxon:191871"
<1..>984
/gene="cyt b"
<1..>984
/gene="cyt b"
/codon_start=1
/transl_table=2
/product="cytochrome b"
/protein_id="AAN45852.1"

/db_xref="GI:24078501"
/translation="MTHLRKSHPLLKIIINHSFIDLPAISNISAAMWFGSLLGVCLIIQ
ILTGLFLAMHYTSDTSTAFSSVAHICRDVNFGLIRNIHANGASMFMCFLHVGRL
YYGSYLFKETWNVGVILLTVMATAFVGVLPGQMSFGATVITNLLSAIPYIGTTL
VEWINGGFSVDKATLTRFAFHFILPFIILALVIVHLLFHETGSNNPTGINPDSDKI
PFHPYYTIKDVGLILMILMLTLALFSPDITLGPDPNFTPANPLNTPPHIKTEWYFLF
AYAILWSIPNKLGGVLLASILVLLINSTLHTSNQWSLMFRPISQTLFWLL"

ORIGIN
Alignment Scores:
Pred. No.: 2.08e+03 Length: 984
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x AF434177 (1-984)

QY 1 IleThrArgAlaArgile 6
|||||
Db 581 ATAACAAGGGCTAGGATA 564

RESULT 33
AX935448

LOCUS AX935448 984 bp DNA linear PAT 05-JAN-2004
DEFINITION Sequence 52 from Patent WO03089475.
ACCESSION AX935448
VERSION AX935448.1 GI:40642196
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
TITLE
Peschen,D., Fischer,R., Schillberg,S., Liao,Y.C. and Dorfmueller,S.
Antibodies, recombinant antibodies, recombinant antibody fragments
and fusions mediated plant disease resistance against fungi
Patent: WO 03089475-A 52 30-OCT-2003;
Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung
e.V. (DE)
JOURNAL
FEATURES
Location/Qualifiers
1..984
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: precursor
fusion protein comprising the RS - linker - scFv CWPD2."

ORIGIN
Alignment Scores:
Pred. No.: 2.08e+03 Length: 984
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x AX935448 (1-984)

QY 1 IleThrArgAlaArgile 6
|||||
Db 59 ATAACGCGTCAAGAATC 76

RESULT 34
AF434176/c

LOCUS AF434176 985 bp DNA linear MAM 17-OCT-2002
DEFINITION Thylamys elegans isolate NK 96571 cytochrome b (cyt b) gene,
partial cds; mitochondrial gene for mitochondrial product.
ACCESSION AF434176
VERSION AF434176.1 GI:24078498
KEYWORDS
SOURCE
ORGANISM
mitochondrion Thylamys elegans (Elegant Fat-tailed Opossum)
Thylamys elegans

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Thylamys. 1 (bases 1 to 985)
AUTHORS Meynard,A.P., Palma,R.E. and Rivera-Milla,E.
TITLE Filogeografia de las llacas chilenas del genero Thylamys (Marsupialia, Didelphidae) en base a secuencias del gen mitochondrial citocromo b
JOURNAL Rev. Chil. Hist. Nat. (2002) In press
REFERENCE 2 (bases 1 to 985)
AUTHORS Meynard,A.P., Palma,R.E. and Rivera-Milla,E.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2001) Ecologia, P. Universidad Catolica de Chile, Casilla 114-D, Santiago, Santiago 6513677, Chile
FEATURES
source Location/Qualifiers
1..985
/organism="Thylamys elegans"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="NK 96571"
/db_xref="taxon:191871"
<1..>985
/gene="cyt b"
<1..>985
/gene="cyt b"
/codon_start=1
/transl_table=2
/product="cytochrome b"
/protein_id="AA045851.1"
/db_xref="GI:24078499"
/translation="MTHLRKSHPLLKIINHSDFLPAPSNISAWNFGSLGVCLLIQ ILTGLFLAMHYTSDTSTAFSSVAHICRDVNFGLIRNIHANGASMFMCFLFHVGRGL YGSYLFKETWNVGVILLVTMATAFVGYVLPWGQMSFWGATVITNLLSAIPYIGTTL VEWIWGFSVDKATLRFFAFHFILPFIILAVIVHLLFLHETGNSNPNPSGINPDSDKI PFHPYYTIKDVGLILMILMLLTALFSPDTLGDPDNFTPANPLNTPPHIKPEWYFLF AYAILWSIPNKLGGVLALLASILVLLASSTTSYIKPTKLNISTNFTNLVLI"

ORIGIN

Alignment Scores: Pred. No.: 2.08e+03 Length: 985
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x AF434176 (1-985)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 581 ATAACAGGCTAGGATA 564

RESULT 35
AX935453
LOCUS AX935453 987 bp DNA linear PAT 05-JAN-2004
DEFINITION Sequence 57 from Patent WO03089475.
ACCESSION AX935453
VERSION AX935453.1 GI:40642201
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Peschen,D., Fischer,R., Schillberg,S., Liao,Y.C. and Dorfmueller,S.
AUTHORS Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease resistance against fungi
TITLE Patent: WO 03089475-A 57 30-OCT-2003;
JOURNAL Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung e.V. (DE)
FEATURES
source Location/Qualifiers
1..987
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores: Pred. No.: 2.09e+03 Length: 987
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-41 (1-6) x AX935453 (1-987)
Qy 1 IleThrArgAlaArgile 6
|||||
Db 59 ATAACGCGTGCAAGAATC 76
RESULT 36
AX935455
LOCUS AX935455 987 bp DNA linear PAT 05-JAN-2004
DEFINITION Sequence 59 from Patent WO03089475.
ACCESSION AX935455
VERSION AX935455.1 GI:40642203
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 Peschen,D., Fischer,R., Schillberg,S., Liao,Y.C. and Dorfmueller,S.
AUTHORS Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease resistance against fungi
TITLE Patent: WO 03089475-A 59 30-OCT-2003;
JOURNAL Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung e.V. (DE)
FEATURES
source Location/Qualifiers
1..987
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: precursor fusion protein comprising RS - linker scFv VDM2."

ORIGIN

Alignment Scores: Pred. No.: 2.09e+03 Length: 987
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x AX935455 (1-987)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 59 ATAACGCGTGCAAGAATC 76

RESULT 37
AF431925/c
LOCUS AF431925 988 bp DNA linear MAM 10-NOV-2002
DEFINITION Thylamys elegans isolate NK 95436 cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product.
ACCESSION AF431925
VERSION AF431925.1 GI:24849957
KEYWORDS
SOURCE mitochondrion Thylamys elegans (Elegant Fat-tailed Opossum)
ORGANISM Thylamys elegans

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Thylamys. 1 (bases 1 to 988)
AUTHORS Eduardo Palma,R., Rivera-Milla,E., Yates,T.L., Marquet,P.A. and Meynard,A.P.

TITLE Phylogenetic and biogeographic relationships of the mouse opossum
Thylamys (Didelphimorphia, Didelphidae) in southern South America
JOURNAL Mol. Phylogenet. Evol. 25 (2), 245-253 (2002)
MEDLINE 22302519
PUBMED 12414307
REFERENCE 2 (bases 1 to 988)
AUTHORS Palma,R.Eduardo., Rivera-Milla,E., Yates,T.L., Marquet,P.A. and
Meynard,A.P.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (11-OCT-2001) Ecologia, P. Universidad Catolica de Chile,
Casilla 114-D, Santiago 6513677, Chile
FEATURES Location/Qualifiers
source 1..988
/organism="Thylamys elegans"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="NK 95436"
/db_xref="taxon:191871"
<1..>988
/gene="cytb"
/gene="cytb"
/codon_start=1
/product="cytochrome b"
/protein_id="AAN64835.1"
/db_xref="GI:24849958"
/translation="MTLRLKSHPLKIIINHSFIDLPA PSNISAWNFGSLGVCILIIQ
ILTGLFLAMHYTSDTSTAFSSVAHICRDVNFGLIRNIHANGASMFMCFLHVGRL
YGSYLFKETWNVGVILLTVMATAFVGYPWGQMSFWGATVITNLLSAIPYIGTTL
VEWINGGFSVDKATLTRFFAFHFILPFIILALVIVHLLFLHETGSNNPTGINPDSDKI
PFHPYYTIKDIILGLILMLLLTALFSPDMLGDPNFTRLTHSMPLPMSKPEWYFLF
AYAILRSIPNKLGGVLLALLASILVLLVPLLLHTSNQSRSLMFRPISQTLFWLLT"
ORIGIN
Alignment Scores:
Pred. No.: 2.09e+03 Length: 988
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-41 (1-6) x AF431925 (1-988)
Qy 1 IleThrArgAlaArgile 6
Db 581 ATAACAGGGCTAGGATA 564
RESULT 38
AF431923/c
LOCUS AF431923 990 bp DNA linear MAM 10-NOV-2002
DEFINITION Thylamys pallidior isolate EP 440 cytochrome b (cytb) gene, partial
cgs; mitochondrial gene for mitochondrial product.
ACCESSION AF431923
VERSION AF431923.1 GI:24849953
KEYWORDS
SOURCE Mitochondrion Thylamys pallidior (pallid fat-tailed opossum)
ORGANISM Thylamys pallidior
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Thylamys.
REFERENCE 1 (bases 1 to 990)
AUTHORS Eduardo Palma,R., Rivera-Milla,E., Yates,T.L., Marquet,P.A. and
Meynard,A.P.
TITLE Phylogenetic and biogeographic relationships of the mouse opossum
Thylamys (Didelphimorphia, Didelphidae) in southern South America
JOURNAL Mol. Phylogenet. Evol. 25 (2), 245-253 (2002)
MEDLINE 22302519
PUBMED 12414307
REFERENCE 2 (bases 1 to 990)
AUTHORS Palma,R.Eduardo., Rivera-Milla,E., Yates,T.L., Marquet,P.A. and
Meynard,A.P.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (11-OCT-2001) Ecologia, P. Universidad Catolica de Chile,
Casilla 114-D, Santiago 6513677, Chile
FEATURES Location/Qualifiers
source 1..990
/organism="Thylamys pallidior"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="EP 440"
/db_xref="taxon:126301"
<1..>990
/gene="cytb"
/gene="cytb"
/codon_start=1
/product="cytochrome b"
/protein_id="AAN64833.1"
/db_xref="GI:24849954"
/translation="MTNLRKSHPLMKIINHSPIDLPA PSNISAWNFGSLGICLIIO
ILTGLFLAMHYTSDTLTAFSSVAHICRDVNFGLIRNIHANGASMFMCFLHVGRL
YGSYLFKETWNVGIVILLTVMATAFVGYPWGQMSFWGATVITNLLSAIPYIGTTL
VEWINGGFSVDKATLTRFFAFHFILPFIILALVIVHLLFLHETGSNNPTGINPDSDKI
PFHPYYTIKDVILGLILMLLLTALFSPDMLGDPDNFTPANPLNTPPHIKPEWYFLF
AYAILRSIPNKLGGVLLALLASILVLLVPLLLHTSNQSRSLMFRPISQTLFWLLTA"
ORIGIN
Alignment Scores:
Pred. No.: 2.09e+03 Length: 990
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-41 (1-6) x AF431923 (1-990)
Qy 1 IleThrArgAlaArgile 6
Db 581 ATAACAGGGCTAGGATA 564
RESULT 39
CQ497388
LOCUS CQ497388 1039 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 29255 from Patent WO0160860.
ACCESSION CQ497388
VERSION CQ497388.1 GI:41463024
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 29255 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
source 1..1039
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2.19e+03 Length: 1039
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-41 (1-6) x CQ497388 (1-1039)

TITLE Phylogenetic and biogeographic relationships of the mouse opossum
Thylamys (Didelphimorphia, Didelphidae) in southern South America
JOURNAL Mol. Phylogenet. Evol. 25 (2), 245-253 (2002)
MEDLINE 22302519
PUBMED 12414307
REFERENCE 2 (bases 1 to 988)
AUTHORS Palma,R.Eduardo., Rivera-Milla,E., Yates,T.L., Marquet,P.A. and
Meynard,A.P.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (11-OCT-2001) Ecologia, P. Universidad Catolica de Chile,
Casilla 114-D, Santiago 6513677, Chile
FEATURES Location/Qualifiers
source 1..990
/organism="Thylamys pallidior"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="EP 440"
/db_xref="taxon:126301"
<1..>990
/gene="cytb"
/gene="cytb"
/codon_start=1
/product="cytochrome b"
/protein_id="AAN64833.1"
/db_xref="GI:24849954"
/translation="MTNLRKSHPLMKIINHSPIDLPA PSNISAWNFGSLGICLIIO
ILTGLFLAMHYTSDTLTAFSSVAHICRDVNFGLIRNIHANGASMFMCFLHVGRL
YGSYLFKETWNVGIVILLTVMATAFVGYPWGQMSFWGATVITNLLSAIPYIGTTL
VEWINGGFSVDKATLTRFFAFHFILPFIILALVIVHLLFLHETGSNNPTGINPDSDKI
PFHPYYTIKDVILGLILMLLLTALFSPDMLGDPDNFTPANPLNTPPHIKPEWYFLF
AYAILRSIPNKLGGVLLALLASILVLLVPLLLHTSNQSRSLMFRPISQTLFWLLTA"
ORIGIN
Alignment Scores:
Pred. No.: 2.09e+03 Length: 990
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-41 (1-6) x AF431923 (1-990)
Qy 1 IleThrArgAlaArgile 6
Db 581 ATAACAGGGCTAGGATA 564
RESULT 39
CQ497388
LOCUS CQ497388 1039 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 29255 from Patent WO0160860.
ACCESSION CQ497388
VERSION CQ497388.1 GI:41463024
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 29255 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
source 1..1039
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2.19e+03 Length: 1039
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101B-41 (1-6) x CQ497388 (1-1039)

Search completed: February 18, 2005, 05:26:06
Job time : 828.72 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2005, 21:47:40 ; Search time 107.16 Seconds
(without alignments)
331.452 Million cell updates/sec

Title: US-10-014-101B-41
Perfect score: 27
Sequence: 1 ITRARI 6

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101_@CGN_1_1_701_@runat_16022005_075845_7925 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	159	10 ADG32304	Adg32304 Radish cd
C 2	27	100.0	192	6 ABN68746	Abn68746 Streptoco
C 3	27	100.0	195	6 ABN70489	Abn70489 Streptoco
4	27	100.0	354	10 ACD94249	Acd94249 Human col
5	27	100.0	375	4 ABA09353	Aba09353 Human sec

C	6	27	100.0	384	8 ABX53359	Abx53359 Bovine ES
	7	27	100.0	493	5 ABV07966	Abv07966 Human pro
	8	27	100.0	503	3 AAC36788	Aac36788 Arabidops
	9	27	100.0	537	6 ABQ24115	Abq24115 Oligonucl
C	10	27	100.0	537	6 ABQ24114	Abq24114 Oligonucl
	11	27	100.0	708	8 ACA21667	Aca21667 Prokaryot
	12	27	100.0	831	2 AAQ99805	Aaq99805 Thaumatin
	13	27	100.0	874	3 AAC69410	Aac69410 Human sec
	14	27	100.0	900	2 AAV32472	Aav32472 Ubiquitin
C	15	27	100.0	936	11 ABD13501	Abd13501 Pseudomon
	16	27	100.0	984	10 ADG32343	Adg32343 DNA encod
	17	27	100.0	987	10 ADG32350	Adg32350 DNA encod
	18	27	100.0	987	10 ADG32348	Adg32348 DNA encod
	19	27	100.0	1039	5 ABV29237	Abv29237 Human pro
	20	27	100.0	1059	10 ADC24030	Adc24030 DNA seque
	21	27	100.0	1059	12 ADH36131	Adh36131 Chemical
	22	27	100.0	1059	12 ADG93832	Adg93832 Nitrilase
	23	27	100.0	1059	12 ADI62429	Adi62429 DNA encod
	24	27	100.0	1059	12 ADI64550	Adi64550 DNA encod
C	25	27	100.0	1124	13 ADS60562	Ads60562 Bacterial
C	26	27	100.0	1171	8 ACA21136	Aca21136 Prokaryot
C	27	27	100.0	1215	8 ACA01962	Aca01962 C. glutam
	28	27	100.0	1290	11 ABD13808	Abd13808 Pseudomon
C	29	27	100.0	1311	11 ABD13579	Abd13579 Pseudomon
C	30	27	100.0	1434	5 AAH65248	Aah65248 C glutami
	31	27	100.0	1436	3 AAC44665	Aac44665 Arabidops
	32	27	100.0	1506	6 ABK28625	Abk28625 cDNA enco
	33	27	100.0	1506	9 ACC85294	Acc85294 Arabidops
	34	27	100.0	1506	10 ADH61267	Adh61267 Arabidops
	35	27	100.0	1506	12 ADO06498	Ado06498 A thalian
	36	27	100.0	1515	6 ABK28629	Abk28629 cDNA enco
	37	27	100.0	1515	9 ACC85298	Acc85298 Arabidops
	38	27	100.0	1539	8 ACA26612	Aca26612 Prokaryot
	39	27	100.0	1548	3 AAC43214	Aac43214 Arabidops
C	40	27	100.0	1564	11 ADL66030	Adl66030 C. glutam
	41	27	100.0	1566	8 ADA71115	Ada71115 Rice gene
	42	27	100.0	1572	6 ABK28626	Abk28626 cDNA enco
	43	27	100.0	1572	9 ACC85295	Acc85295 Arabidops
	44	27	100.0	1572	10 ADH61268	Adh61268 Arabidops
	45	27	100.0	1575	3 AAC42983	Aac42983 Arabidops

ALIGNMENTS

RESULT 1
ADG32304
ID ADG32304 standard; cDNA; 159 BP.
XX
AC ADG32304;
XX
DT 26-FEB-2004 (first entry)
XX
DE Radish cDNA encoding an antifungal protein (AFP) SeqID 13.
XX
KW radish; scfV; gene; ss; anti-fungal peptide; AFP; scfV;
KW disease resistant; transgenic; plant; fungal infection; antibody;
KW pathogen-specific antibody; fungicidal; agriculture.
XX
OS Raphanus sativus.
XX
PN WO2003089475-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-EP003852.
XX
PR 22-APR-2002; 2002EP-00008929.
PR 28-MAY-2002; 2002EP-00011807.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
XX

DR WPI; 2003-854088/79.
DR P-PSDB; ADG32329.
XX
PT New fusion protein comprising an anti-fungal protein or peptide and an
PT antibody fragment, useful in agriculture and horticulture for producing
PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
PS Claim 26; SEQ ID NO 13; 47pp; English.
XX
CC This invention relates to a novel fusion protein comprising an anti-
CC fungal protein or peptide (AFP) and an antibody fragment (scFv).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
CC and a cellular targeting sequence, which can be used to generate disease
CC resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in
CC plants such that the undesirable and expensive chemical controls often
CC used in agriculture are not required. The present invention provides
CC antibodies, recombinant antibodies and fragments thereof, as well as
CC fusion proteins that can be used as pathogen-specific antibodies targeted
CC to different plant cell compartments. As such, these fungicidal agents
CC confer a broad spectrum of disease resistance in both economically
CC important crops and ornamental plants. This polynucleotide is a cDNA
CC sequence encoding an antifungal protein of the invention.
XX
SQ Sequence 159 BP; 42 A; 32 C; 42 G; 43 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 526 Length: 159
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-41 (1-6) x ADG32304 (1-159)

QY 1 IleThrArgAlaArgIle 6
Db 59 ATAACGCGTGCAAGATC 76
|||||

RESULT 2

ABN68746/c
ID ABN68746 standard; DNA; 192 BP.

XX AC ABN68746;

XX DT 01-JUL-2002 (first entry)

DE Streptococcus polynucleotide SEQ ID NO 5405.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX Streptococcus agalactiae.

XX WO200234771-A2.

XX PN 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB004789.

XX PR 27-OCT-2000; 2000GB-00026333.

XX PR 24-NOV-2000; 2000GB-00028727.

XX PR 07-MAR-2001; 2001GB-00005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;

XX PI Tettelin H;

XX WPI; 2002-352536/38.

DR P-PSDB; ABP28115.

XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.

XX PS Claim 7; Page 3702; 4525pp; English.

XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins

XX SQ Sequence 192 BP; 56 A; 29 C; 42 G; 65 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 647 Length: 192
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x ABN68746 (1-192)

QY 1 IleThrArgAlaArgIle 6
Db 116 ATAACAAGAGCAAGATT 99
|||||

RESULT 3

ABN70489/c

ID ABN70489 standard; DNA; 195 BP.

XX AC ABN70489;

XX DT 01-JUL-2002 (first entry)

DE Streptococcus polynucleotide SEQ ID NO 8891.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

XX Streptococcus agalactiae.

XX WO200234771-A2.

XX PN 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB004789.

XX PR 27-OCT-2000; 2000GB-00026333.

XX PR 24-NOV-2000; 2000GB-00028727.

XX PR 07-MAR-2001; 2001GB-00005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;

XX PI Tettelin H;

XX WPI; 2002-352536/38.
DR P-PSDB; ABP29858.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 7; Page 4007; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 195 BP; 58 A; 29 C; 42 G; 66 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 658 Length: 195
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x ABN70489 (1-195)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 116 ATAACAAGAGCAAGAATT 99

RESULT 4
ACD94249
ID ACD94249 standard; cDNA; 354 BP.
XX
AC ACD94249;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #2661.
XX

KW Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PF 27-SEP-1999; 99US-00406117.
XX
PR 20-NOV-1998; 98US-00196716.
XX

PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.

PA (BREN/) BRENTANI R R.
XX
PI Simpson AJG, Neto ED, Brentani RR;
XX
DR WPI; 2003-182626/18.
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
XX Example 9; Page 400; 959pp; English.
XX
CC The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX
SQ Sequence 354 BP; 66 A; 100 C; 113 G; 74 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 1.27e+03 Length: 354
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-41 (1-6) x ACD94249 (1-354)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 277 ATTACCCGAGCGCAATT 294

RESULT 5
ABAA09353
ID ABAA09353 standard; cDNA; 375 BP.
XX
AC ABAA09353;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:1129.
XX

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB12109.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 1; Page 916; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 375 BP; 73 A; 133 C; 101 G; 68 T; 0 U; 0 Other;
Alignment Scores: Length: 375
Pred. No.: 1.35e+03 Matches: 6
Score: 27.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 4
US-10-014-101B-41 (1-6) x ABA09353 (1-375)
QY 1 IleThrArgAlaArgIle 6
Db 224 ATCACGAGAGCTAGAATA 241
RESULT 6
ID ABX53359/c
XX ABX53359 standard; cDNA; 384 BP.
AC ABX53359;
XX
DT 25-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #3288.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137160-A1.
XX
PD 26-SEP-2002.
XX
PF 26-OCT-2001; 2001US-00983965.
XX
PR 17-DEC-1998; 98US-0113678P.
PR 15-DEC-1999; 99US-00465231.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-102386/09.
XX
PT Purified nucleic acid molecules, useful for genome mapping, gene
PT identification and analysis, cattle breeding or preparation of constructs
PT for cattle gene expression and genetically improved cattle.
XX
PS Claim 2; SEQ ID NO 3288; 38pp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
CC appearing as ABX50072-ABX55983, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 5912 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the

CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137160

XX SQ Sequence 384 BP; 123 A; 58 C; 75 G; 128 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.38e+03 Length: 384
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x ABX53359 (1-384)

Qy 1 IleThrArgAlaArgile 6
Db 330 ATAACCAGAGCTCGGATA 313

RESULT 7
ABV07966
ID ABV07966 standard; cDNA; 493 BP.
XX
AC ABV07966;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 7957.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183319P.

XX 16-MAR-2000; 2000US-0189862P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 1275; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the

CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 493 BP; 125 A; 104 C; 77 G; 132 T; 0 U; 55 Other;

Alignment Scores:
Pred. No.: 1.82e+03 Length: 493
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-41 (1-6) x ABV07966 (1-493)

Qy 1 IleThrArgAlaArgile 6
Db 98 ATTACCCGTGCCCGGATA 115

RESULT 8
AAC36788
ID AAC36788 standard; DNA; 503 BP.
XX
AC AAC36788;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15080.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 30-APR-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 06-MAY-1999; 99US-0132487P.

XX 07-MAY-1999; 99US-0132863P.

XX 11-MAY-1999; 99US-0134256P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

Tue Feb 22 10:19:08 2005

PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.

PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159233P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1.86e+03 Length: 503
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AAC36788 (1-503)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 104 ATAACGAGAGCCAGATT 121

RESULT 9
ABQ24115
ID ABQ24115 standard; DNA; 537 BP.
XX
AC ABQ24115;
XX
DT 12-JUL-2002 (first entry)
XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 10706.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
DR
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central

CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX

SQ Sequence 537 BP; 192 A; 204 C; 49 G; 92 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2e+03 Length: 537
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x ABQ24115 (1-537)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 240 ATAACCCGCGCAGATA 257

RESULT 10
ABQ24114/c
ID ABQ24114 standard; DNA; 537 BP.
XX
AC ABQ24114;
XX
DT 12-JUL-2002 (first entry)
XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 10705.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
DR
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:

CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 537 BP; 92 A; 49 C; 204 G; 192 T; 0 U; 0 Other;

Alignment Scores: 2e+03 Length: 537
Pred. No.: 27.00 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x ABQ24114 (1-537)

QY 1 IleThrArgAlaArgile 6
Db 298 ATAAACCGCGCAGCAATA 281

RESULT 11
ACA21667
ID ACA21667 standard; DNA; 708 BP.
XX
AC ACA21667;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #3324.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Bacillus anthracis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU17797.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 9537; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 708 BP; 273 A; 85 C; 155 G; 195 T; 0 U; 0 Other;

Alignment Scores: 2.71e+03 Length: 708
Pred. No.: 27.00 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x ACA21667 (1-708)

QY 1 IleThrArgAlaArgile 6
Db 150 ATTACAAGAGCGAGGATA 167

RESULT 12
AAQ99805
ID AAQ99805 standard; cDNA; 831 BP.
XX
AC AAQ99805;
XX
DT 20-JUN-1996 (first entry)
XX
DE Thaumatin like gene PR-5mz.
XX
KW SAR; tobacco; protein-synthesis independent gene; cyclohexamide;
KW systemic acquired resistance response; anti-pathogen; plant protection;
KW maize; PR-5; ss.
XX
KW Zea mays.
OS
XX
FH Key Location/Qualifiers
FT CDS 72..590
FT /*tag= a
XX
XX WO9519443-A2.
PN
XX
PD 20-JUL-1995.
XX
XX 03-JAN-1995; 95WO-IB0000002.
PF
XX 13-JAN-1994; 94US-00181271.
PR
XX (CIBA) CIBA GEIGY AG.
PA
XX

PI Ryals JA, Alexander DC, Uknes SJ, Ward ER;
XX WPI; 1995-263872/34.
DR P-PSDB; AAR81082.
DR
XX
PT New DNA contg. plant systemic acquired resistance genes - and transgenic
PT plants contg. them, impart disease and pest resistance, also Arabidopsis
PT gene promoter to control DNA transcription.
XX
PS Claim 21; Page 72-73; 85pp; English.
XX
CC This sequence represents the DNA sequence of a maize thaumatin like gene,
CC PR-5mz. This sequence was isolated by screening a BTH-induced cDNA
CC library of maize, with a probe matching a known rice thaumatin clone.
CC This sequence, and AAQ99800-Q99804 are all used in recombinant/chimaeric
CC DNA molecules of the invention. These sequences were isolated by
CC differential screening of a cDNA library, followed by analysis by
CC Northern hybridisation to RNA in the presence and absence of
CC cyclohexamide. The genes are used in the creation of transgenic plants.
CC All of these sequences confer anti-pathogenic properties to transgenic
CC plants. Transgenic expression of 2 or more of the recombinant molecules
CC of the invention that encode anti-pathogenic proteins provides a
CC synergistic increase in plant protection, and may also offer protection
CC against a wider range of pathogens
XX
SQ Sequence 831 BP; 182 A; 259 C; 230 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.23e+03 Length: 831
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x AAQ99805 (1-831)

QY 1 IleThrArgAlaArgIle 6
Db 684 ATTACACGTGCACGCATT 701

RESULT 13
AAC69410
ID AAC69410 standard; cDNA; 874 BP.
XX
AC AAC69410;
XX
XX 30-JAN-2001 (first entry)
XX
DE Human secreted protein gene 12 SEQ ID NO:22.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cyostatic; cardiant; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; skin aging; food additive; preservative; ss.
XX
OS Homo sapiens.
XX
XX WO2000058468-A2.
PN
XX
PD 05-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US007526.
XX
PR 26-MAR-1999; 99US-0126600P.
PR 22-DEC-1999; 99US-0171550P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-611713/58.
DR P-PSDB; AAB38130.
XX
PT Nucleic acids encoding human secreted proteins, used to prevent, treat,
PT ameliorate, or diagnose conditions such as autoimmune disorders, skin
PT disorders and cancer.
XX
PS Claim 1; Page 323-324; 374pp; English.
XX
CC The polynucleotide sequences given in AAC69399 to AAC69445 encode the
CC human secreted proteins given in AAB38119 to AAB38165. AAB38166 to
CC AAB38201 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
CC cyostatic; cardiant; vasotropic; cerebroprotective; neurotropic;
CC neuroprotective; antibacterial; virucide; fungicide; and
CC ophthalmological. The polynucleotides and polypeptides can be are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC autoimmune diseases, hyperproliferative disorders, cardiovascular
CC disorders, cerebrovascular disorders, angiogenesis, nervous system
CC disorders, infections caused by bacteria, viruses and fungi and ocular
CC disorders. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. AAC69390 to AAC69398 and
CC AAB38118 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 874 BP; 237 A; 216 C; 232 G; 185 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 3.42e+03 Length: 874
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AAC69410 (1-874)

QY 1 IleThrArgAlaArgIle 6
Db 717 ATACACAGGGCTAGATA 734

RESULT 14
AAV32472
ID AAV32472 standard; DNA; 900 BP.
XX
AC AAV32472;
XX
DT 17-OCT-2003 (revised)
DT 10-SEP-1998 (first entry)
XX
DE Ubiquitin gene of Mamestra brassicae nuclear polyhedrosis virus.
XX
KW Ubiquitin gene; ds.
XX
OS Mamestra brassicae nucleopolyhedrovirus.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..405 /*tag= b
FT promoter 1..40 /*tag= a
FT FT 406..708
FT CDS

FT /*tag= c
FT /product= "Ubiquitin"
FT 709. .900
FT /*tag= d

PN JP10150989-A.
XX
PD 09-JUN-1998.
XX
PF 26-NOV-1996; 96JP-00315069.
XX
PR 26-NOV-1996; 96JP-00315069.
XX
PA (NOYA-) NOYAKU BIOTECHNOLOGY KAIHATSU.
XX
DR WPI; 1998-379992/33.
DR P-PSDB; AAW48856.

PT DNA coding ubiquitin from Mamestra brassicae nuclear polyhedrosis virus
PT - used to detect Mamestra brassicae nuclear polyhedrosis virus.

XX Claim 2; Page 5-6; 7pp; Japanese.

XX The invention claims for the Mamestra brassicae nuclear polyhedrosis
CC virus ubiquitin gene and the protein it encodes. The ubiquitin gene can
CC be used as an index to detect the Mamestra brassicae nuclear
CC polyhedrosis virus. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 900 BP; 301 A; 175 C; 171 G; 253 T; 0 U; 0 Other;

Alignment Scores: Length: 900
Pred. No.: 3.53e+03 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x AAV32472 (1-900)

QY 1 IleThrArgAlaArgile 6
DB 656 ATAACCCGGCTCGAATA 673

RESULT 15
ABD13501/c
ID ABD13501 standard; DNA; 936 BP.

XX ABD13501;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #12105.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR P-PSDB; ABO79930.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 12105; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html

XX Sequence 936 BP; 151 A; 321 C; 319 G; 145 T; 0 U; 0 Other;

Alignment Scores: Length: 936
Pred. No.: 3.68e+03 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-41 (1-6) x ABD13501 (1-936)

QY 1 IleThrArgAlaArgile 6
DB 333 ATCACCAGGGCGGATC 316

RESULT 16
ADG32343
ID ADG32343 standard; DNA; 984 BP.

XX ADG32343;

XX 26-FEB-2004 (first entry)

XX DNA encoding the precursor fusion protein AFP RS-scfV CWPD2 SeqID 52.

XX radish; scfV; ds; anti-fungal peptide; AFP; scfV; disease resistant;
KW transgenic; plant; fungal infection; antibody;
KW pathogen-specific antibody; fungicidal; agriculture; chimeric; chicken;
KW gene.

XX Chimeric.

XX Synthetic.

XX Raphanus sativus.

XX Gallus gallus.

XX WO2003089475-A2.

XX 30-OCT-2003.

XX 14-APR-2003; 2003WO-EP003852.

XX 22-APR-2002; 2002EP-00008929.

XX 28-MAY-2002; 2002EP-00011807.

XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;

PI

XX WPI; 2003-854088/79.
DR P-PSDB; ADG32354.
XX
PT New fusion protein comprising an anti-fungal protein or peptide and an
PT antibody fragment, useful in agriculture and horticulture for producing
PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
PS Example 4; SEQ ID NO 52; 47pp; English.
XX
CC This invention relates to a novel fusion protein comprising an anti-
CC fungal protein or peptide (AFP) and an antibody fragment (scFV).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
CC and a cellular targeting sequence, which can be used to generate disease
CC resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in
CC plants such that the undesirable and expensive chemical controls often
CC used in agriculture are not required. The present invention provides
CC antibodies, recombinant antibodies and fragments thereof, as well as
CC fusion proteins that can be used as pathogen-specific antibodies targeted
CC to different plant cell compartments. As such, these fungicidal agents
CC confer a broad spectrum of disease resistance in both economically
CC important crops and ornamental plants. This polynucleotide is a DNA
CC sequence encoding a precursor fusion protein of the order [AFP - linker -
CC antibody fragment] of the invention.
XX
SQ Sequence 984 BP; 204 A; 270 C; 310 G; 200 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.89e+03 Length: 984
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-41 (1-6) x ADG32343 (1-984)

Qy 1 IleThrArgAlaArgIle 6
Db 59 ATAACGCGTGCAAGAATC 76

RESULT 17
ADG32350
ID ADG32350 standard; DNA; 987 BP.
XX
AC ADG32350;
XX
DT 26-FEB-2004 (first entry)
XX
DE DNA encoding the precursor fusion protein of AFP RS-scFV VDM2 SeqID 59.
XX
KW radish; scFV; ds; anti-fungal peptide; AFP; scFV; disease resistant;
KW transgenic; plant; fungal infection; antibody;
KW pathogen-specific antibody; fungicidal; agriculture; mouse; chimeric;
KW murine; gene.
XX
OS Chimeric.
OS Synthetic.
OS Raphanus sativus.
OS Mus musculus.
XX
PN WO2003089475-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-EP003852.
XX
PR 22-APR-2002; 2002EP-00008929.
PR 28-MAY-2002; 2002EP-00011807.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX

PI Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
XX WPI; 2003-854088/79.
DR P-PSDB; ADG32361.
XX
PT New fusion protein comprising an anti-fungal protein or peptide and an
PT antibody fragment, useful in agriculture and horticulture for producing
PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
PS Example 15; SEQ ID NO 59; 47pp; English.
XX
CC This invention relates to a novel fusion protein comprising an anti-
CC fungal protein or peptide (AFP) and an antibody fragment (scFV).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
CC and a cellular targeting sequence, which can be used to generate disease
CC resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in
CC plants such that the undesirable and expensive chemical controls often
CC used in agriculture are not required. The present invention provides
CC antibodies, recombinant antibodies and fragments thereof, as well as
CC fusion proteins that can be used as pathogen-specific antibodies targeted
CC to different plant cell compartments. As such, these fungicidal agents
CC confer a broad spectrum of disease resistance in both economically
CC important crops and ornamental plants. This polynucleotide is a DNA
CC sequence encoding a precursor fusion protein of the order [AFP - linker -
CC antibody fragment] of the invention.
XX
SQ Sequence 987 BP; 252 A; 225 C; 268 G; 242 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.9e+03 Length: 987
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-41 (1-6) x ADG32350 (1-987)

Qy 1 IleThrArgAlaArgIle 6
Db 59 ATAACGCGTGCAAGAATC 76

RESULT 18
ADG32348
ID ADG32348 standard; DNA; 987 BP.
XX
AC ADG32348;
XX
DT 26-FEB-2004 (first entry)
XX
DE DNA encoding the precursor fusion protein of AFP RS-scFV VDCw SeqID 57.
XX
KW radish; scFV; ds; anti-fungal peptide; AFP; scFV; disease resistant;
KW transgenic; plant; fungal infection; antibody;
KW pathogen-specific antibody; fungicidal; agriculture; mouse; chimeric;
KW murine; gene.
XX
OS Chimeric.
OS Synthetic.
OS Raphanus sativus.
OS Mus musculus.
XX
PN WO2003089475-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-EP003852.
XX
PR 22-APR-2002; 2002EP-00008929.
PR 28-MAY-2002; 2002EP-00011807.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX

XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
PI WPI; 2003-854088/79.
XX P-PSDB; ADG32359.
DR
XX New fusion protein comprising an anti-fungal protein or peptide and an
PT antibody fragment, useful in agriculture and horticulture for producing
PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
PS Example 15; SEQ ID NO 57; 47pp; English.
XX
CC This invention relates to a novel fusion protein comprising an anti-
CC fungal protein or peptide (AFP) and an antibody fragment (scFv).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
CC and a cellular targeting sequence, which can be used to generate disease
CC resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in
CC plants such that the undesirable and expensive chemical controls often
CC used in agriculture are not required. The present invention provides
CC antibodies, recombinant antibodies and fragments thereof, as well as
CC fusion proteins that can be used as pathogen-specific antibodies targeted
CC to different plant cell compartments. As such, these fungicidal agents
CC confer a broad spectrum of disease resistance in both economically
CC important crops and ornamental plants. This polynucleotide is a DNA
CC sequence encoding a precursor fusion protein of the order [AFP - linker -
CC antibody fragment] of the invention.
XX
SQ Sequence 987 BP; 249 A; 228 C; 271 G; 239 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.9e+03 Length: 987
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-41 (1-6) x ADG32348 (1-987)

QY 1 IleThrArgAlaArgile 6
Db 59 ATAACGGCGTGAAGAATC 76

RESULT 19
ABV29237
ID ABV29237 standard; cDNA; 1039 BP.
XX
AC ABV29237;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 29228.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
DR
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 6234-6235; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynanamic or pharmacogenomic marker
XX
SQ Sequence 1039 BP; 294 A; 276 C; 280 G; 188 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 4.13e+03 Length: 1039
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-41 (1-6) x ABV29237 (1-1039)

QY 1 IleThrArgAlaArgile 6
Db 892 ATTACGAGGCGACGAATA 909

RESULT 20
ADC24030
ID ADC24030 standard; DNA; 1059 BP.
XX
AC ADC24030;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA sequence (SeqID 297) encoding a nitrilase enzyme.
XX
KW gene; ds; nitrilase; nitrile; cyanohydrin; ammonia; biocatalyst;
KW enantiomer; chiral medicine.
XX
OS Unidentified.
XX
PN WO2003000840-A2.
XX
PD 03-JAN-2003.
XX
PF 15-MAY-2002; 2002WO-US015983.
XX
PR 21-JUN-2001; 2001US-0300189P.
PR 30-JUL-2001; 2001US-0309006P.
PR 22-JAN-2002; 2002US-0351336P.
XX
PA (DIVE-) DIVERSA CORP.
PA (MADD/) MADDEN D.
XX
PI Madden M, Desantis G, Chaplin JA, Weiner DP, Milan A, Chi E;
PI Short JM, Burk M;
XX
DR WPI; 2003-201417/19.
DR P-PSDB; ADC24031.

XX Novel nitrilase polypeptide, useful for making (R)- or (S)-ethyl-4-cyano-
PT 3-hydroxybutyric acid or (R)- or (S)-mandelic acid or (S)- or (R)-phenyl
PT lactic acid derivative and for producing pharmaceutical composition, and
PT food additive.
XX
PS Claim 1; SEQ ID NO 297; 560pp; English.
XX
CC This invention relates to nitrilases and the nucleic acids that encode
CC these enzymes thereof. Specifically, it refers to polypeptides that
CC exhibit nitrilase activity, i.e. the ability to directly hydrolyse
CC nitriles or cyanohydrins into their corresponding carboxylic acids and
CC ammonia. Nitrilases have commercial utility as biocatalysts for use in
CC the synthesis of enantiomerically pure aromatic and aliphatic amino
CC acids, as well as hydroxy acids, which are important for the development
CC of chiral medicines. Furthermore, the present invention describes
CC nitrilases, isolated from mesophilic microorganisms, that have improved
CC activity and stability at increased pH and temperature. They are also
CC inexpensive, efficient catalysts, have broad substrate specificity and
CC are capable of chiral differentiation. This polynucleotide is a DNA
CC sequence that encodes a nitrilase enzyme of the invention.
XX
SQ Sequence 1059 BP; 202 A; 322 C; 346 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.22e+03 Length: 1059
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-014-101B-41 (1-6) x ADC24030 (1-1059)

Qy 1 IleThrArgAlaArgIle 6
Db 884 ATTACTCGCGCCGGATA 901
|||||

RESULT 21
ADH36131
ID ADH36131 standard; DNA; 1059 BP.
XX
AC ADH36131;
XX
DT 11-MAR-2004 (first entry)
XX
DE Chemical process monitoring-related nitrilase gene sequence SeqID297.
XX
KW Chemical process monitoring; biochemical process monitoring; cyanide;
KW high throughput system; gene; ds.
XX
OS Unidentified.
XX
PN WO2003098187-A2.
XX
PD 27-NOV-2003.
XX
PF 15-MAY-2003; 2003WO-US015639.
XX
PR 15-MAY-2002; 2002US-0380737P.

XX (DIVE-) DIVERSA CORP.
XX Weiner D, Chaplin JA, Chi E, Milan A, Desantis G, Burk MJ;
PI Mcquaid J, Stege J;
XX
DR WPI; 2004-142708/14.
DR P-PSDB; ADH36132.
XX
PT Monitoring a chemical or biochemical process comprises providing a
PT reactant comprising a cyanide or a material that can be converted to
PT cyanide or a reactant that generates a cyanide or a material that can be
PT converted to cyanide.

XX Claim 74; SEQ ID NO 297; 277pp; English.
PS
XX
CC This invention relates to a novel method of monitoring chemical or
CC biochemical processes. The method involves providing a reactant
CC comprising cyanide (or a material that can be converted to a cyanide)
CC that generates as a reaction product cyanide or a material that can be
CC converted to cyanide and measuring the concentration of produced cyanide.
CC The method is useful for monitoring a chemical or biochemical process.
CC The method is effective for high throughput systems and is sufficiently
CC sensitive to detect a small amount of product. The present sequence is
CC that of a gene which encodes a nitrilase enzyme which can be used in the
CC method of the invention.

XX Sequence 1059 BP; 202 A; 322 C; 346 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.22e+03 Length: 1059
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-41 (1-6) x ADH36131 (1-1059)

Qy 1 IleThrArgAlaArgIle 6
Db 884 ATTACTCGCGCCGGATA 901
|||||

RESULT 22
ADG93832
ID ADG93832 standard; DNA; 1059 BP.
XX
AC ADG93832;
XX
DT 11-MAR-2004 (first entry)
XX
DE Nitrilase enzyme gene sequence SeqID297.
XX
KW nitrilase; nitrile; carboxylic acid; chemical process; pH; temperature;
KW enantioselective transformation; gene; ds.
XX
OS Unidentified.
XX
PN WO2003097810-A2.
XX
PD 27-NOV-2003.
XX
PF 15-MAY-2003; 2003WO-US015712.
XX
PR 15-MAY-2002; 2002US-00146772.
PR 09-SEP-2002; 2002US-00241742.

XX (DIVE-) DIVERSA CORP.
XX Desantis G, Short JM, Burk M, Wong K, Farwell R, Chatman K;
PI
XX WPI; 2004-090637/09.
DR P-PSDB; ADG93833.
XX
PT New isolated or recombinant nucleic acid encoding a polypeptide having
PT nitrilase activity, useful for screening enantioselective transformation.
XX
PS Claim 44; SEQ ID NO 297; 295pp; English.

XX This invention is related to a novel isolated or recombinant nucleic acid
CC encoding a protein having nitrilase activity. Nitrilase's are capable of
CC converting nitrile's directly to carboxylic acids and have great
CC potential for use in industrial chemical processes. The isolated
CC nitrilase proteins of the invention have increased activity and stability
CC at increased pH and temperature when compared to those conventionally
CC used. In addition, the nucleic acid of the invention is useful for

CC screening enantioselective transformation. The present sequence is that
CC of a DNA sequence which encodes a nitrilase enzyme of the invention.
XX
SQ Sequence 1059 BP; 202 A; 322 C; 346 G; 189 T; 0 U; 0 Other;
Alignment Scores: Length: 1059
Pred. No.: 4.22e+03 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-014-101B-41 (1-6) x ADG93832 (1-1059)
QY 1 IleThrArgAlaArgIle 6
Db 884 ATTACTCGCGCCCGGATA 901
RESULT 23
ADI62429
ID ADI62429 standard; DNA; 1059 BP.
XX
AC ADI62429;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA encoding nitrilase polypeptide #149.
XX
KW Atorvastatin; (R)-ethyl 4-cyano-3-hydroxybutyrate;
KW (R)-ethyl 4-cyano-3-hydroxybutyric acid; epichlorohydrin;
KW 3-hydroxyglutaronitrile; 3-hydroxyglutaronitrile;
KW 4-cyano-3-hydroxybutyric acid; ethyl-4-cyano-3-hydroxybutyric acid;
KW mixed hyperlipidaemia; homozygous familial hypercholesterolaemia;
KW antilipaemic; gene; ds.
XX
OS Unidentified.
XX
PN WO2003106415-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-US018840.
XX
PR 13-JUN-2002; 2002US-0389317P.
PR 28-JUN-2002; 2002US-0392944P.
XX
PA (DIVE-) DIVERSA CORP.
XX
PI Burk M, Desantis G, Morgan B, Zhu Z;
XX
DR WPI; 2004-090821/09.
DR P-PSDB; ADI62430.
XX
PT Preparation of atorvastatin comprises catalytic conversion of 3-
PT hydroxyglutaronitrile by polypeptide with nitrilase activity, converting
PT obtained 4-cyano-3-hydroxybutyric acid to ethyl-4-cyano-3-hydroxybutyric
PT acid and forming atorvastatin.
XX
PS Claim 46; SEQ ID NO 297; 253pp; English.
XX
CC The present invention relates to a method for preparing an atorvastatin
CC intermediate known as (R)-ethyl 4-cyano-3-hydroxybutyrate ((R)-ethyl 4-
CC cyano-3-hydroxybutyric acid). The method comprises optionally converting
CC epichlorohydrin or equivalent to 3-hydroxyglutaronitrile, catalytic
CC conversion of 3-hydroxyglutaronitrile or equivalent to 4-cyano-3-
CC hydroxybutyric acid with a polypeptide having nitrilase activity,
CC converting 4-cyano-3-hydroxybutyric to ethyl-4-cyano-3-hydroxybutyric
CC acid, and converting this to (R)-ethyl 4-cyano-3-hydroxybutyrate. The
CC method involves whole cell processes, cell lysate process, "one pot"
CC processes, and "multi-pot" processes using a variety of parameters.
CC Atorvastatin is used, in conjunction with dietary restriction, in the
CC management of hyperlipidaemia, including hypercholesterolaemia, mixed

CC dyslipidaemia and homozygous familial hypercholesterolaemia. The present
CC sequence encodes a nitrilase polypeptide obtained from an environmental
CC sample.
XX
SQ Sequence 1059 BP; 202 A; 322 C; 346 G; 189 T; 0 U; 0 Other;
Alignment Scores: Length: 1059
Pred. No.: 4.22e+03 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-014-101B-41 (1-6) x ADI62429 (1-1059)
QY 1 IleThrArgAlaArgIle 6
Db 884 ATTACTCGCGCCCGGATA 901
RESULT 24
ADI64550
ID ADI64550 standard; DNA; 1059 BP.
XX
AC ADI64550;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA encoding nitrilase seq id 149.
XX
KW (R)-ethyl 4-cyano-3-hydroxybutyric acid; nitrile hydrolysis;
KW carboxylic acid; cyanohydrin moiety hydrolysis;
KW aminonitrile moiety hydrolysis; chiral alpha-hydroxy acid molecule;
KW chiral amino acid molecule; (S)-ethyl 4-cyano-3-hydroxybutyric acid;
KW (R)-mandelic acid; (S)-mandelic acid; (S)-phenyl lactic acid derivative;
KW (R)-phenyl lactic acid derivative; & enantiomeric excess;
KW & diastomeric excess; food additive; drug intermediate; ds; nitrilase;
KW gene.
XX
OS Unidentified.
XX
PN US2004014195-A1.
XX
PD 22-JAN-2004.
XX
PF 15-MAY-2003; 2003US-00440523.
XX
PR 29-DEC-1999; 99US-0173609P.
PR 07-DEC-2000; 2000US-0254414P.
PR 28-DEC-2000; 2000US-00751299.
PR 21-JUN-2001; 2001US-0300189P.
PR 30-JUL-2001; 2001US-0309006P.
PR 22-JAN-2002; 2002US-0351336P.
PR 15-MAY-2002; 2002US-00146772.
PR 09-SEP-2002; 2002US-00241742.
XX
PA (DIVE-) DIVERSA CORP.
XX
PI Desantis G, Short JM, Burk MJ, Wong K, Farwell R, Chatman K;
XX
DR WPI; 2004-121569/12.
DR P-PSDB; ADI64551.
XX
PT Novel isolated or recombinant polypeptide having nitrilase activity,
PT useful in production of food additives.
XX
PS Claim 1; SEQ ID NO 297; 105pp; English.
XX
CC The invention describes an isolated or recombinant polypeptide (I)
CC comprising amino acids having a sequence at least 50 % identical to a
CC sequence (S1) available in electronic form (EC) from the following web
CC site ftp.segdata.uspto.gov/sequence.html?DocID=2004014195, or its
CC variants, having one or more mutations at residue 55 Lys, Gly or Glu, at

CC residue 60 glutamic acid, at residue 111 Ser, their combinations or
CC fragments. (I) is useful for: producing an (R)-ethyl 4-cyano-3-
CC hydroxybutyric acid; hydrolysing a nitrile to a carboxylic acid;
CC hydrolysing cyanohydrin moiety or an aminonitrile moiety; producing a
CC chiral alpha-hydroxy acid molecule or a chiral amino acid molecule;
CC producing an (S)-ethyl 4-cyano-3-hydroxybutyric acid; producing an (R)-
CC mandelic acid or (S)-mandelic acid; producing (S)-phenyl lactic acid
CC derivative or an (R)-phenyl lactic acid derivative; modifying a molecule;
CC and for identifying a modified compound. The inventive method is useful
CC for monitoring or determining % enantiomeric excess or % diastomeric
CC excess. (I) is useful in the production of food additives and drug
CC intermediates. This sequence encodes a nitrilase of the invention.
XX
SQ Sequence 1059 BP; 202 A; 322 C; 346 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.22e+03 Length: 1059
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-014-101B-41 (1-6) x ADI64550 (1-1059)

Qy 1 IleThrArgAlaArgIle 6
Db 884 ATTACTCGCGCCGGATA 901
|||||

RESULT 25
ADS60562/c
ID ADS60562 standard; cDNA; 1124 BP.

XX
AC ADS60562;

XX
DT 02-DEC-2004 (first entry)

XX
DE Bacterial polynucleotide #12549.

KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.

XX
OS Bacteria.

XX
PN US2003233675-A1.

XX
PD 18-DEC-2003.

XX
PF 20-FEB-2003; 2003US-00369493.

XX
PR 21-FEB-2002; 2002US-0360039P.

XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX
DR WPI; 2004-061375/06.

XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX
PS Claim 1; SEQ ID NO 36236; 122pp; English.

XX

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 1124 BP; 260 A; 326 C; 284 G; 254 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.5e+03 Length: 1124
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-41 (1-6) x ADS60562 (1-1124)

Qy 1 IleThrArgAlaArgIle 6
|||||

Db 1010 ATCACTAGAGCGGAATC 993
|||||

RESULT 26

ACA21136/c

ID ACA21136 standard; DNA; 1171 BP.

XX
AC ACA21136;

XX
DT 19-JUN-2003 (first entry)

XX
DE Prokaryotic essential gene #2793.

XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.

XX
OS Acinetobacter baumannii.

XX
PN WO200277183-A2.

XX
PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.

XX
PR 21-MAR-2001; 2001US-00815242.

XX
PR 06-SEP-2001; 2001US-00948993.

XX
PR 25-OCT-2001; 2001US-0342923P.

XX
PR 08-FEB-2002; 2002US-00072851.

XX
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.
DR P-PSDB; ABU17266.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 9006; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1171 BP; 368 A; 146 C; 165 G; 492 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.71e+03 Length: 1171
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x ACA21136 (1-1171)

QY 1 IleThrArgAlaArgIle 6
DB 422 ATTACAAGAGCTCGGATC 405

RESULT 27
ACA01962/c
ID ACA01962 standard; DNA; 1215 BP.
XX
AC ACA01962;
XX
DT 04-JUN-2003 (first entry)
XX
DE C. glutamicum derived ORF SEQ ID 1953.
XX
KW Coryneform; nucleic acid array; fermentation; culture; ds.
XX
OS Corynebacterium glutamicum.
XX
PN DE10128510-A1.
XX

PD 19-DEC-2002.
XX
PF 13-JUN-2001; 2001DE-01028510.
XX
PR 13-JUN-2001; 2001DE-01028510.
XX
PA (DEGS) DEGUSSA AG.
XX
PI Farwick M, Moeckel B, Pfefferle W, Bathe B, Huthmacher K;
XX
DR WPI; 2003-279970/28.
XX
PT New nucleic acid array useful for monitoring mRNA expression of
PT Corynebacterium glutamicum during fermentation, comprising nucleic acid
PT from Corynebacterium glutamicum.
XX
PS Claim 1; Page 645-646; 709pp; German.
XX
CC This invention describes a novel nucleic acid array involving
CC Corynebacterium glutamicum polynucleotides. The arrays are used to
CC analyse C. glutamicum, particularly for monitoring a fermentation process
CC to determine expression levels of C. glutamicum cellular mRNA. Such
CC monitoring particularly differentiates between expression levels of
CC different strains of C. glutamicum and allows the adjustment of different
CC culture and fermentation conditions. ACA00010-ACA02188 represent C.
CC glutamicum derived polynucleotides described in the disclosure of the
CC invention
XX
SQ Sequence 1215 BP; 319 A; 248 C; 298 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.91e+03 Length: 1215
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x ACA01962 (1-1215)

QY 1 IleThrArgAlaArgIle 6
DB 284 ATCACAGGGCAGCATC 267

RESULT 28
ABD13808
ID ABD13808 standard; DNA; 1290 BP.
XX
AC ABD13808;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #12412.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.

DR P-PSDB; ABO80237.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 12412; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1290 BP; 193 A; 434 C; 451 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.24e+03 Length: 1290
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-41 (1-6) x ABD13808 (1-1290)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 935 ATCACCAGGCGGAGGATC 952

RESULT 29
ABD13579/c
ID ABD13579 standard; DNA; 1311 BP.
XX
AC ABD13579;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #12183.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO80008.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 12183; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1311 BP; 220 A; 456 C; 443 G; 192 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.33e+03 Length: 1311
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-41 (1-6) x ABD13579 (1-1311)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 416 ATCACCAGGCGGAGGATC 399

RESULT 30
AAH65248/c
ID AAH65248 standard; DNA; 1434 BP.
XX
AC AAH65248;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 283.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG90029.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing

PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 283; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 1434 BP; 381 A; 291 C; 360 G; 402 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.88e+03 Length: 1434
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-014-101B-41 (1-6) x AAH65248 (1-1434)

QY 1 IleThrArgAlaArgIle 6
Db 503 ATCAACAAGGCACGCATC 486

RESULT 31
ID AAC44665
XX AAC44665 standard; DNA; 1436 BP.
AC AAC44665;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43666.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.

PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.

PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 5.89e+03 Length: 1436
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x AAC44665 (1-1436)

QY 1 IleThrArgAlaArgIle 6
Db 1087 ATTACAAGGGCGAGGATT 1104

RESULT 32
ABK28625
ID ABK28625 standard; cDNA; 1506 BP.
XX
AC ABK28625;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX2.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2002-130736/17.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 146-147; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production

CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention

XX SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores: Length: 1506
Pred. No.: 6.21e+03 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x ABK28625 (1-1506)

QY 1 IleThrArgAlaArgIle 6
DB 646 ATAACGAGAGCCAGAATT 663

RESULT 33

ACC85294
ID ACC85294 standard; cDNA; 1506 BP.

AC ACC85294;

XX 18-SEP-2003 (first entry)

DT Arabidopsis cytokinin oxidase-like protein 2 cDNA.

DE Maize; root growth; root geotropism; cytokinin oxidase; seed size;
XX embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

XX Arabidopsis thaliana.

OS WO2003050287-A2.

XX 19-JUN-2003.

PF 10-DEC-2002; 2002WO-EP013990.

XX 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2003-541577/51.

XX Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

XX Claim 3; Page 167-168; 177pp; English.

XX The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level

CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention

XX SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores: Length: 1506
Pred. No.: 6.21e+03 Matches: 6
Score: 27.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-41 (1-6) x ACC85294 (1-1506)

QY 1 IleThrArgAlaArgIle 6
DB 646 ATAACGAGAGCCAGAATT 663

RESULT 34

ADH61267
ID ADH61267 standard; DNA; 1506 BP.

XX AC ADH61267;

XX 25-MAR-2004 (first entry)

XX Arabidopsis thaliana cytokinin oxidase (CKX1) DNA #1.

DE Male-sterility; cytokinin oxidase; transgenic plant; seed production;
XX CKX1; mouse-ear cress; gene; ds.

XX Arabidopsis thaliana.

XX US2003163847-A1.

XX 28-AUG-2003.

XX 20-DEC-2002; 2002US-00326184.

XX 20-DEC-2001; 2001US-0343129P.

XX (PHAA) PHARMACIA CORP.

XX Huang S, Crossland LD, Cheikh N, Morris RO;

XX WPI; 2003-897983/82.

DR GENBANK; AF303978.

XX Producing plants characterized by reversible male-sterility, useful for
PT maintaining male sterility in plants, by transforming a plant cell with a
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT nucleic acid construct containing a polynucleotide encoding a cytokinin
PT oxidase.

XX Claim 41; SEQ ID NO 8; 33pp; English.

XX The invention relates to a method for producing a plant characterised by
CC reversible male-sterility which involves transforming a plant cell with a
CC nucleic acid construct containing a polynucleotide encoding a cytokinin
CC oxidase. The method is useful for producing reversible male-sterility in
CC transgenic plants, or for maintaining male sterility in plants. The
CC method reduces the expense of seed production for existing hybrid plants
CC such as corn, but also makes it possible to produce hybrid varieties of
CC traditionally non-hybrid crops. The method is also useful for introducing
CC economically valuable traits from plants having undesirable production

CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention

XX
SQ Sequence 1515 BP; 456 A; 327 C; 378 G; 354 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.25e+03 Length: 1515
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x ABK28629 (1-1515)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 673 ATACGCGGCAAGAATA 690

RESULT 37
ACC85298
ID ACC85298 standard; cDNA; 1515 BP.
XX
AC ACC85298;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 6 cDNA.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FN WO2003050287-A2.
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmulling T, Werner T;
XX
DR WPI; 2003-541577/51.
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

XX
PS Claim 2; Page 171-172; 177pp; English.
XX

CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or

CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention

XX
SQ Sequence 1515 BP; 456 A; 327 C; 378 G; 354 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.25e+03 Length: 1515
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-41 (1-6) x ACC85298 (1-1515)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 673 ATACGCGGCAAGAATA 690

RESULT 38
ACA26612
ID ACA26612 standard; DNA; 1539 BP.
XX
AC ACA26612;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #8269.
XX

KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Burkholderia mallei.
XX
FN WO200277183-A2.
PD 03-OCT-2002.
XX

PF 21-MAR-2002; 2002WO-US0009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX

PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX

DR WPI; 2003-029926/02.
DR P-PSDB; ABU22742.

XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX
PS Claim 14; SEQ ID NO 14482; 1766pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1539 BP; 197 A; 514 C; 605 G; 223 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.36e+03 Length: 1539
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x ACA26612 (1-1539)

Qy 1 IleThrArgAlaArgile 6
Db 1136 ATCACACGCGCGGCATC 1153

RESULT 39

AAC43214
ID AAC43214 standard; DNA; 1548 BP.

XX
AC AAC43214;

XX
DT 17-OCT-2000 (first entry)

XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX
OS Arabidopsis thaliana.

XX
PN EP1033405-A2.

XX
PD 06-SEP-2000.

XX
PF 25-FEB-2000; 2000EP-00301439.

XX
PR 25-FEB-1999; 99US-0121825P.

PR
PR 05-MAR-1999; 99US-0123180P.

PR
PR 09-MAR-1999; 99US-0123548P.

PR
PR 23-MAR-1999; 99US-0125788P.

PR
PR 25-MAR-1999; 99US-0126264P.

PR
PR 29-MAR-1999; 99US-0126785P.

PR
PR 01-APR-1999; 99US-0127462P.

PR
PR 06-APR-1999; 99US-0128234P.

PR
PR 08-APR-1999; 99US-0128714P.

PR
PR 16-APR-1999; 99US-0129845P.

PR
PR 19-APR-1999; 99US-0130077P.

PR
PR 21-APR-1999; 99US-0130449P.

PR
PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.

XX This invention describes novel polynucleotides that encode protein
CC markers and fine chemical-production proteins from *Corynebacterium*
CC glutamicum. The polynucleotides are isolated from a nucleic acid library
CC of *C. glutamicum* then mutated at the specified positions, cloned and
CC expressed by standard methods. Cells, especially *Corynebacterium*
CC glutamicum, containing vectors that express the polynucleotides are used
CC for production of fine chemicals, preferably amino acids and specifically
CC lysine, but more generally nucleotides, nucleosides, lipids, fatty acids,
CC diols, carbohydrates, aromatic compounds, vitamins, co-factors and
CC enzymes. These are useful in the food, animal feed, cosmetics and
CC pharmaceutical industries. The polynucleotides, optionally as primers and
CC probes, can also be used for identification and classification of *C.*
CC glutamicum and related species, e.g. for diagnosis, for genomic mapping,
CC functional or evolutionary studies, gene manipulation and modulation of
CC metabolic activity. Cells that containing the polynucleotides of the
CC invention may produce fine chemicals in better yields, with higher
CC productivity and/or more efficiently. NOTE: This sequence is not
CC represented in the printed specification but is available in electronic
CC format. The sequence represented in this record has been obtained from
CC WO2003046123.
XX
SQ Sequence 1564 BP; 416 A; 314 C; 396 G; 438 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.47e+03 Length: 1564
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-014-101B-41 (1-6) x ADL66030 (1-1564)

Qy 1 ILeThrArgAlaArgIle 6
Db 603 ATCACAAGGGCAGCATC 586

Search completed: February 18, 2005, 03:27:13
Job time : 112.16 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 02:33:38 ; Search time 35.4 Seconds
(without alignments)
277.335 Million cell updates/sec

Title: US-10-014-101B-41
Perfect score: 27
Sequence: 1 ITRARI 6

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database : Issued Patents_NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	1290	4 US-09-252-991A-12412	Sequence 12412, A
C 3	27	100.0	1311	4 US-09-252-991A-12183	Sequence 12183, A
4	27	100.0	1605	3 US-09-124-541-3	Sequence 3, Appli
5	27	100.0	1605	4 US-09-663-326-3	Sequence 3, Appli
6	27	100.0	1839	2 US-08-915-207-3	Sequence 3, Appli
7	27	100.0	1839	3 US-09-238-555-3	Sequence 3, Appli
8	27	100.0	1842	2 US-08-915-207-1	Sequence 1, Appli
9	27	100.0	1842	3 US-09-238-555-1	Sequence 1, Appli
10	27	100.0	2013	4 US-09-614-221A-614	Sequence 614, App
11	27	100.0	2875	1 US-08-328-314-1	Sequence 1, Appli
12	27	100.0	2875	1 US-08-731-045-1	Sequence 1, Appli

13	27	100.0	6733	3 US-09-124-541-2	Sequence 2, Appli
14	27	100.0	6733	4 US-09-663-326-2	Sequence 2, Appli
C 15	27	100.0	11014	4 US-08-956-171E-91	Sequence 91, Appl
C 16	27	100.0	11014	4 US-08-781-986A-91	Sequence 91, Appl
17	27	100.0	29771	4 US-09-949-016-12754	Sequence 12754, A
18	27	100.0	29771	4 US-09-949-016-13956	Sequence 13956, A
19	27	100.0	70014	4 US-09-949-016-17110	Sequence 17110, A
C 20	27	100.0	141115	4 US-09-949-016-17490	Sequence 17490, A
C 21	26	96.3	75	3 US-08-671-824-20	Sequence 20, Appl
C 22	26	96.3	75	4 US-09-686-341-16	Sequence 16, Appl
23	26	96.3	185	4 US-09-313-294A-2688	Sequence 2688, Ap
C 24	26	96.3	283	4 US-09-313-294A-3534	Sequence 3534, Ap
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26	26	96.3	297	4 US-09-313-294A-4423	Sequence 4423, Ap
C 27	26	96.3	473	4 US-09-270-767-5082	Sequence 5082, Ap
C 28	26	96.3	473	4 US-09-270-767-20364	Sequence 20364, A
29	26	96.3	601	4 US-09-949-016-33777	Sequence 33777, A
C 30	26	96.3	601	4 US-09-949-016-44357	Sequence 44357, A
C 31	26	96.3	601	4 US-09-949-016-44358	Sequence 44358, A
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33	26	96.3	601	4 US-09-949-016-52246	Sequence 52246, A
C 34	26	96.3	601	4 US-09-949-016-60727	Sequence 60727, A
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36	26	96.3	601	4 US-09-949-016-110977	Sequence 110977,
37	26	96.3	601	4 US-09-949-016-111138	Sequence 111138,
38	26	96.3	601	4 US-09-949-016-111299	Sequence 111299,
39	26	96.3	601	4 US-09-949-016-150894	Sequence 150894,
40	26	96.3	714	3 US-08-998-416-867	Sequence 867, App
C 41	26	96.3	798	4 US-09-252-991A-7733	Sequence 7733, Ap
C 42	26	96.3	1165	4 US-09-949-016-5024	Sequence 5024, Ap
C 43	26	96.3	1176	4 US-09-252-991A-11843	Sequence 11843, A
C 44	26	96.3	2073	3 US-09-221-017B-894	Sequence 894, App
C 45	26	96.3	2103	4 US-09-252-991A-11773	Sequence 11773, A

ALIGNMENTS

RESULT 1

US-09-252-991A-12105/c
; Sequence 12105, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12105
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12105

Alignment Scores:	1.26e+03	Length: 936
Pred. No.:	27.00	Matches: 6
Score:	100.00%	Conservative: 0
Percent Similarity:	100.00%	Mismatches: 0
Best Local Similarity:	100.00%	Indels: 0
Query Match:	100.00%	Gaps: 0
DB:	4	

US-10-014-101B-41 (1-6) x US-09-252-991A-12105 (1-936)

OY 1 IletHrArgAlaArgile 6

Db 333 ATCACCAGGGCGAGGATC 316

RESULT 2

US-09-252-991A-12412
; Sequence 12412, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12412
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12412

Alignment Scores:
Pred. No.: 1.76e+03 Length: 1290
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-252-991A-12412 (1-1290)

QY 1 IleThrArgAlaArgile 6
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Db 935 ATCACCAGGCGGAGGATC 952

RESULT 3

US-09-252-991A-12183/c
; Sequence 12183, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12183
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12183

Alignment Scores:
Pred. No.: 1.79e+03 Length: 1311
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-252-991A-12183 (1-1311)

QY 1 IleThrArgAlaArgile 6
|||||
Db 416 ATCACCAGGCGGAGGATC 399

RESULT 4

US-09-124-541-3
; Sequence 3, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-124-541-3

Alignment Scores:
Pred. No.: 2.21e+03 Length: 1605
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-124-541-3 (1-1605)

QY 1 IleThrArgAlaArgile 6
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Db 703 ATCACCAGGCGGCGGATC 720

RESULT 5

US-09-663-326-3
; Sequence 3, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-663-326-3

Alignment Scores:
Pred. No.: 2.21e+03 Length: 1605
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-663-326-3 (1-1605)

QY 1 IleThrArgAlaArgile 6
|||||
Db 703 ATCACCAGGCGGCGGATC 720

RESULT 6
US-08-915-207-3
; Sequence 3, Application US/08915207
; Patent No. 5882897
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K.R.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NOVEL YitJ
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,207
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1839 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd Q
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: P50549-3
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1839 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-915-207-3

Alignment Scores:
Pred. No.: 2.54e+03 Length: 1839
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x US-08-915-207-3 (1-1839)
Qy 1 IleThrArgAlaArgIle 6
| | | | | | | | | | | | | | | | | | | |
Db 651 ATTACCAGACGACGCATT 668

RESULT 7
US-09-238-555-3
; Sequence 3, Application US/09238555
; Patent No. 6251652
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K.R.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NOVEL YitJ
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia

STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,555
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,207
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1839 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-238-555-3

Alignment Scores:
Pred. No.: 2.54e+03 Length: 1839
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-238-555-3 (1-1839)
Qy 1 IleThrArgAlaArgIle 6
| | | | | | | | | | | | | | | | | | | |
Db 651 ATTACCAGACGACGCATT 668

RESULT 8
US-08-915-207-1
; Sequence 1, Application US/08915207
; Patent No. 5882897
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K.R.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NOVEL YitJ
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,207
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd Q
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: P50549-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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US-08-915-207-1
;
Alignment Scores:
Pred. No.: 2.55e+03 1842
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 2 0
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US-10-014-101B-41 (1-6) x US-08-915-207-1 (1-1842)
QY 1 IleThrArgAlaArgile 6
Db 651 ATTACCAGACGCGCATT 668
;
RESULT 9
US-09-238-555-1
; Sequence 1, Application US/09238555
; Patent No. 6251652
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K.R.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NOVEL YitJ
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/238,555
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/915,207
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd Q
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: P50549-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: linear
;
US-09-238-555-1
;
Alignment Scores:
Pred. No.: 2.55e+03 1842
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 3 0
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US-10-014-101B-41 (1-6) x US-09-238-555-1 (1-1842)
QY 1 IleThrArgAlaArgile 6
Db 651 ATTACCAGACGCGCATT 668
;
RESULT 10
US-09-614-221A-614
; Sequence 614, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 614
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
;
US-09-614-221A-614
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Alignment Scores:
Pred. No.: 2.79e+03 2013
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 4 0
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US-10-014-101B-41 (1-6) x US-09-614-221A-614 (1-2013)
QY 1 IleThrArgAlaArgile 6
Db 228 ATTACCCGTGCCCCGAATT 245
;
RESULT 11
US-08-328-314-1
; Sequence 1, Application US/08328314
; Patent No. 5674728
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
; APPLICANT: Jarai, Gabor
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: Fungal Protease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,314
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-19746/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger N400
; STRAIN: Aspergillus niger N400
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1269..1370, 1462..1612, 1669..2323, 2382
; LOCATION: ..2667)
; OTHER INFORMATION: /function= "Aspartic Protease"
; OTHER INFORMATION: /product= "PEPE"
; OTHER INFORMATION: /gene= "pepE"
; FEATURE:
; NAME/KEY: intron
; LOCATION: order(1371..1461, 1613..1668, 2324..2381)
; FEATURE:
; NAME/KEY: exon
; LOCATION: join(1269..1370, 1462..1612, 1669..2323, 2382
; LOCATION: ..2667)
; US-08-328-314-1

Alignment Scores:
Pred. No.: 4.05e+03 Length: 2875
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-41 (1-6) x US-08-328-314-1 (1-2875)

Qy 1 IleThrArgAlaArgile 6
Db 788 ATCACC CGCGCTCGGATT 805

RESULT 12
US-08-731-045-1
; Sequence 1, Application US/08731045
; Patent No. 5756338
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
; APPLICANT: Jarai, Gabor
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: Fungal Protease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY CORPORATION
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9725
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/731,045
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/328,314
; FILING DATE: October 24, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 4-19746/A/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-3318
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger N400
; STRAIN: Aspergillus niger N400
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1269..1370, 1462..1612, 1669..2323, 2382
; LOCATION: ..2667)
; OTHER INFORMATION: /function= "Aspartic Protease"
; OTHER INFORMATION: /product= "PEPE"
; OTHER INFORMATION: /gene= "pepE"
; FEATURE:
; NAME/KEY: intron
; LOCATION: order(1371..1461, 1613..1668, 2324..2381)
; FEATURE:
; NAME/KEY: exon
; LOCATION: join(1269..1370, 1462..1612, 1669..2323, 2382
; LOCATION: ..2667)
; US-08-731-045-1

Alignment Scores:
Pred. No.: 4.05e+03 Length: 2875
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-41 (1-6) x US-08-731-045-1 (1-2875)

Qy 1 IleThrArgAlaArgile 6
Db 788 ATCACC CGCGCTCGGATT 805

RESULT 13
US-09-124-541-2
; Sequence 2, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
```



```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-124-541-2

Alignment Scores:
Pred. No.:          9.8e+03      Length:    6733
Score:              27.00       Matches:     6
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:        100.00%     Indels:      0
DB:                  3         Gaps:         0

US-10-014-101B-41 (1-6) x US-09-124-541-2 (1-6733)

Qy      1   IleThrArgAlaArgIle 6
           ||| ||||| ||||| ||||| |||
Db      2611 ATCACCGGGCCGATC 2628

RESULT 14
US-09-663-326-2
; Sequence 2, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: MORRIS Ph.D., ROY O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-663-326-2

Alignment Scores:
Pred. No.:          9.8e+03      Length:    6733
```


US-09-949-016-17110
; Sequence 17110, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17110
; LENGTH: 70014
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(70014)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17110

Alignment Scores:
Pred. No.: 1.09e+05 Length: 70014
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-17110 (1-70014)
Qy 1 IleThrArgAlaArgile 6
Db 31410 ATACTAGGCAAGAATT 31427

RESULT 20
US-09-949-016-17490/c
; Sequence 17490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17490
; LENGTH: 141115
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(141115)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17490

Alignment Scores:
Pred. No.: 2.21e+05 Length: 141115

Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-17490 (1-141115)
Qy 1 IleThrArgAlaArgile 6
Db 59860 ATCAAGAGCCCGGATC 59843

RESULT 21
US-08-671-824-20/c
; Sequence 20, Application US/08671824
; Patent No. 6025167
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Zaug, Arthur J.
; APPLICANT: Been, Michael D.
; TITLE OF INVENTION: RNA RIBOZYME POLYMERASES,
; TITLE OF INVENTION: DEPHOSPHORYLASES, RESTRICTION
; TITLE OF INVENTION: ENDORIBONUCLEASES AND METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,824
; FILING DATE: June 5, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,624
; FILING DATE: July 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 220/166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-671-824-20

Alignment Scores:
Pred. No.: 161 Length: 75
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x US-08-671-824-20 (1-75)
Qy 1 IleThrArgAlaArgile 6
:::|||||

```
Db      33 GTTACCCGAGCTCGAATT 16

RESULT 22
US-09-686-341-16/c
; Sequence 16, Application US/09686341
; Patent No. 6696250
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Zaig, Arthur J.
; APPLICANT: Been, Michael D.
; TITLE OF INVENTION: RNA RIBOZYME POLYMERASES, DEPHOSPHORYLASES, RESTRICTION
; TITLE OF INVENTION: ENDORIBONUCLEASES AND METHODS
; FILE REFERENCE: MBH00-983-G
; CURRENT APPLICATION NUMBER: US/09/686,341
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/005,325
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: 08/671,824
; PRIOR FILING DATE: 1996-06-05
; PRIOR APPLICATION NUMBER: 08/278,624
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: 07/843,737
; PRIOR FILING DATE: 1992-02-28
; PRIOR APPLICATION NUMBER: 07/562,672
; PRIOR FILING DATE: 1990-08-03
; PRIOR APPLICATION NUMBER: 06/937,327
; PRIOR FILING DATE: 1986-12-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 75
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
; OTHER INFORMATION: nucleic acid molecule.
US-09-686-341-16

Alignment Scores:
Pred. No.:      161      Length:      75
Score:          26.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:     96.30% Indels: 0
DB:              4      Gaps: 0

US-10-014-101B-41 (1-6) x US-09-686-341-16 (1-75)

Qy      1 IleThrArgAlaArgile 6
      ::::::::::::::::::::
Db      33 GTTACCCGAGCTCGAATT 16

RESULT 23
US-09-313-294A-2688
; Sequence 2688, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 2688
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700553119H1

US-10-014-101B-41 (1-6) x US-09-313-294A-2688 (1-185)

Qy      1 IleThrArgAlaArgile 6
      ::::::::::::::::::::
Db      55 ATCACTAGACGACCGTA 72

RESULT 24
US-09-313-294A-3534/c
; Sequence 3534, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3534
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700611809H1

US-09-313-294A-3534

Alignment Scores:
Pred. No.:      640      Length:      283
Score:          26.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:     96.30% Indels: 0
DB:              4      Gaps: 0

US-10-014-101B-41 (1-6) x US-09-313-294A-3534 (1-283)

Qy      1 IleThrArgAlaArgile 6
      ::::::::::::::::::::
Db      23 ATCACCCTGCGCGAGTG 6

RESULT 25
US-09-313-294A-7329
; Sequence 7329, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7329
; LENGTH: 291
; TYPE: DNA
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700553119H1
```



```
; SEQ ID NO 33777
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-33777

Alignment Scores:
Pred. No.:      1.4e+03      Length:      601
Score:          26.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 83.33% Mismatches:    0
Query Match:    96.30%      Indels:      0
DB:              4          Gaps:          0

US-10-014-101B-41 (1-6) x US-09-949-016-33777 (1-601)

Qy      1 IleThrArgAlaArgIle 6
Db      83 ATCACAAAGGCGCGGTGTG 100

RESULT 30
US-09-949-016-44357/c
; Sequence 44357, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44357
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44357

Alignment Scores:
Pred. No.:      1.4e+03      Length:      601
Score:          26.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 83.33% Mismatches:    0
Query Match:    96.30%      Indels:      0
DB:              4          Gaps:          0

US-10-014-101B-41 (1-6) x US-09-949-016-44357 (1-601)

Qy      1 IleThrArgAlaArgIle 6
Db      418 ATTACAAAGGCGCTAGAGTA 401

RESULT 31
US-09-949-016-44358/c
; Sequence 44358, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44358
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44358

Alignment Scores:
Pred. No.:      1.4e+03      Length:      601
Score:          26.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 83.33% Mismatches:    0
Query Match:    96.30%      Indels:      0
DB:              4          Gaps:          0

US-10-014-101B-41 (1-6) x US-09-949-016-44358 (1-601)

Qy      1 IleThrArgAlaArgIle 6
Db      401 ATTACAAAGGCGCTAGAGTA 384

RESULT 32
US-09-949-016-52245
; Sequence 52245, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52245
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-52245

Alignment Scores:
Pred. No.:      1.4e+03      Length:      601
Score:          26.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 83.33% Mismatches:    0
Query Match:    96.30%      Indels:      0
DB:              4          Gaps:          0

US-10-014-101B-41 (1-6) x US-09-949-016-52245 (1-601)

Qy      1 IleThrArgAlaArgIle 6
Db      354 GTGACTCGAGCCAGGATC 371

RESULT 33
US-09-949-016-52246
; Sequence 52246, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52246
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-52246

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-52246 (1-601)

Qy 1 IleThrArgAlaArgIle 6
Db 188 GTGACTCGAGCCAGGATC 205

RESULT 34

US-09-949-016-60727/c
; Sequence 60727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60727
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60727

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-60727 (1-601)

Qy 1 IleThrArgAlaArgIle 6
Db 283 ATCACAGGGCTAGAGTA 266

RESULT 35

US-09-949-016-110816
; Sequence 110816, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110816
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110816

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-110816 (1-601)

Qy 1 IleThrArgAlaArgIle 6
Db 523 GTCACAAGGGCTCGTATT 540

RESULT 36

US-09-949-016-110977
; Sequence 110977, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110977
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110977

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-110977 (1-601)

Qy 1 IleThrArgAlaArgIle 6
Db 523 GTCACAAGGGCTCGTATT 540

RESULT 37
US-09-949-016-111138
; Sequence 111138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111138
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-111138

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-111138 (1-601)

QY 1 IleThrArgAlaArgile 6
:::|||||
Db 523 GTCACAAGGGCTCGTATT 540

RESULT 38
US-09-949-016-111299
; Sequence 111299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111299
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-111299

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-111299 (1-601)
QY 1 IleThrArgAlaArgile 6
:::|||||
Db 523 GTCACAAGGGCTCGTATT 540
RESULT 39
US-09-949-016-150894
; Sequence 150894, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150894
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150894

Alignment Scores:
Pred. No.: 1.4e+03 Length: 601
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x US-09-949-016-150894 (1-601)

QY 1 IleThrArgAlaArgile 6
|||||
Db 83 ATCACAAGGGCCCGTGTG 100

RESULT 40
US-08-998-416-867
; Sequence 867, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jergen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 867:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG154SRP
US-08-998-416-867

Alignment Scores:
Pred. No.: 1.68e+03 Length: 714
Score: 26.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.30% Indels: 0
DB: 3 Gaps: 0

US-10-014-101B-41 (1-6) x US-08-998-416-867 (1-714)

Qy 1 IleThrArgAlaArgile 6
Db 439 GTCACCAGGGCGAGGATT 456

Search completed: February 18, 2005, 07:19:22
Job time : 55.65 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 05:26:14 ; Search time 282.84 Seconds
(without alignments)
125.382 Million cell updates/sec

Title: US-10-014-101B-41
Perfect score: 27
Sequence: 1 ITRARI 6

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Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10014101@cgn_1_1_659@runat_16022005_075848_8061
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	27	100.0	174	18	US-10-425-115-9138	Sequence 9138, Ap
2	27	100.0	175	18	US-10-437-963-10568	Sequence 10568, A
3	27	100.0	217	17	US-10-424-599-106272	Sequence 106272, A
C 4	27	100.0	269	18	US-10-425-115-23471	Sequence 23471, A
C 5	27	100.0	351	18	US-10-425-115-91752	Sequence 91752, A
6	27	100.0	369	18	US-10-425-115-74928	Sequence 74928, A
7	27	100.0	375	17	US-10-276-774-1129	Sequence 1129, Ap
C 8	27	100.0	384	9	US-09-983-965-3288	Sequence 3288, Ap
9	27	100.0	393	17	US-10-424-599-86559	Sequence 86559, A
C 10	27	100.0	406	18	US-10-437-963-34746	Sequence 34746, A
C 11	27	100.0	408	18	US-10-425-115-111568	Sequence 111568, A
C 12	27	100.0	463	18	US-10-425-115-110170	Sequence 110170, A
13	27	100.0	493	18	US-10-357-930-7957	Sequence 7957, Ap
14	27	100.0	524	17	US-10-424-599-32616	Sequence 32616, A
C 15	27	100.0	537	18	US-10-363-345A-10705	Sequence 10705, A
16	27	100.0	537	18	US-10-363-345A-10706	Sequence 10706, A
17	27	100.0	588	18	US-10-425-115-94827	Sequence 94827, A
18	27	100.0	624	18	US-10-437-963-18174	Sequence 18174, A
C 19	27	100.0	685	13	US-10-027-632-23732	Sequence 23732, A
C 20	27	100.0	685	17	US-10-027-632-23732	Sequence 23732, A
21	27	100.0	694	17	US-10-425-114-33876	Sequence 33876, A
22	27	100.0	694	18	US-10-425-115-35576	Sequence 35576, A
23	27	100.0	708	17	US-10-282-122A-9537	Sequence 9537, Ap
24	27	100.0	721	17	US-10-425-114-2055	Sequence 2055, Ap
25	27	100.0	737	13	US-10-027-632-21005	Sequence 21005, A
26	27	100.0	737	17	US-10-027-632-21005	Sequence 21005, A
C 27	27	100.0	750	15	US-10-156-761-5459	Sequence 5459, Ap
28	27	100.0	755	18	US-10-425-115-183342	Sequence 183342, A
29	27	100.0	807	17	US-10-425-114-15687	Sequence 15687, A
30	27	100.0	808	17	US-10-425-114-14429	Sequence 14429, A
31	27	100.0	840	18	US-10-425-115-35579	Sequence 35579, A
32	27	100.0	869	18	US-10-425-115-65670	Sequence 65670, A
33	27	100.0	890	18	US-10-425-115-51212	Sequence 51212, A
34	27	100.0	916	18	US-10-437-963-100905	Sequence 100905, A
35	27	100.0	955	18	US-10-425-115-35581	Sequence 35581, A
36	27	100.0	975	18	US-10-437-963-63753	Sequence 63753, A
37	27	100.0	996	18	US-10-425-115-65672	Sequence 65672, A
38	27	100.0	1023	18	US-10-425-115-65676	Sequence 65676, A
C 39	27	100.0	1027	17	US-10-424-599-87248	Sequence 87248, A
40	27	100.0	1033	17	US-10-425-114-32335	Sequence 32335, A
41	27	100.0	1039	18	US-10-357-930-29255	Sequence 29255, A
42	27	100.0	1043	18	US-10-425-115-65669	Sequence 65669, A
43	27	100.0	1059	15	US-10-146-772-297	Sequence 297, App
44	27	100.0	1059	17	US-10-241-742-297	Sequence 297, App
45	27	100.0	1059	17	US-10-440-523-297	Sequence 297, App

ALIGNMENTS

RESULT 1

US-10-425-115-9138/c
; Sequence 9138, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 9138
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_108328C.1
US-10-425-115-9138

Alignment Scores: 726 Length: 174
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 18

US-10-014-101B-41 (1-6) x US-10-425-115-9138 (1-174)

Qy 1 IleThrArgAlaArgile 6
Db 122 ATTACACGGGCCCGCATT 105

RESULT 2

US-10-437-963-10568
; Sequence 10568, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 10568

; LENGTH: 175

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_16877C.1

US-10-437-963-10568

Alignment Scores: 730 Length: 175
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 18

US-10-014-101B-41 (1-6) x US-10-437-963-10568 (1-175)

Qy 1 IleThrArgAlaArgile 6
Db 46 ATTACAAGAGCTAGGATA 63

RESULT 3

US-10-424-599-106272
; Sequence 106272, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 106272
; LENGTH: 217
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_66981C.1
US-10-424-599-106272

Alignment Scores: 899 Length: 217
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 17

US-10-014-101B-41 (1-6) x US-10-424-599-106272 (1-217)

Qy 1 IleThrArgAlaArgile 6
Db 52 ATAACAAGAGCAAGAATT 69

RESULT 4

US-10-425-115-23471/c
; Sequence 23471, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 23471

; LENGTH: 269

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_121411C.1

US-10-425-115-23471

Alignment Scores: 1.11e+03 Length: 269
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 18

US-10-014-101B-41 (1-6) x US-10-425-115-23471 (1-269)

Qy 1 IleThrArgAlaArgile 6
Db 29 ATCACTAGAGCTCGAATT 12

RESULT 5

US-10-425-115-91752/c
; Sequence 91752, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326.
; SEQ ID NO 91752
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_183673C.1
US-10-425-115-91752

Alignment Scores:
Pred. No.: 1.43e+03 351
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 18 0

US-10-014-101B-41 (1-6) x US-10-425-115-91752 (1-351)

Qy 1 IleThrArgAlaArgile 6
Db 22 ATTACACGTGCGCGCATT 5

RESULT 6

US-10-425-115-74928
; Sequence 74928, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 74928
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_168330C.1
US-10-425-115-74928

Alignment Scores:
Pred. No.: 1.5e+03 369
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 18 0

US-10-014-101B-41 (1-6) x US-10-425-115-74928 (1-369)

Qy 1 IleThrArgAlaArgile 6
Db 107 ATAACGCGCGCGGATC 124

RESULT 7

US-10-276-774-1129
; Sequence 1129, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1129
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-1129

Alignment Scores:
Pred. No.: 1.52e+03 375
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 17 0

US-10-014-101B-41 (1-6) x US-10-276-774-1129 (1-375)

Qy 1 IleThrArgAlaArgile 6
Db 224 ATCACGAGAGCTAGATA 241

RESULT 8

US-09-983-965-3288/c
; Sequence 3288, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 3288
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 30-LIB3058-052-Q1-K1-H5
US-09-983-965-3288

Alignment Scores:
Pred. No.: 1.56e+03 384
Score: 27.00 6
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 9 0

US-10-014-101B-41 (1-6) x US-09-983-965-3288 (1-384)

Qy 1 IleThrArgAlaArgile 6
Db 330 ATAACCAGAGCTCGGATA 313

RESULT 9

US-10-424-599-86559
; Sequence 86559, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 86559
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49174C.1
US-10-424-599-86559

Alignment Scores:
Pred. No.: 1.59e+03 Length: 393
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-424-599-86559 (1-393)

QY 1 IleThrArgAlaArgIle 6
Db 92 ATTACACGGCGCAGGATC 109

RESULT 10

US-10-437-963-34746/c
; Sequence 34746, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 34746
; LENGTH: 406

; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38731C.1

US-10-437-963-34746

Alignment Scores:
Pred. No.: 1.64e+03 Length: 406
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-437-963-34746 (1-406)

QY 1 IleThrArgAlaArgIle 6
Db 239 ATAACTCGGCGCGCATC 222

RESULT 11

US-10-425-115-111568/c

; Sequence 111568, Application US/10425115

; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 111568
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33238C.1
US-10-425-115-111568

Alignment Scores:
Pred. No.: 1.65e+03 Length: 408
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-111568 (1-408)

QY 1 IleThrArgAlaArgIle 6
Db 21 ATTACACGGCGCGCATC 4

RESULT 12

US-10-425-115-110170/c

; Sequence 110170, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 110170

; LENGTH: 463

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_31970C.1

US-10-425-115-110170

Alignment Scores:
Pred. No.: 1.87e+03 Length: 463
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-110170 (1-463)

QY 1 IleThrArgAlaArgIle 6
Db 21 ATTACACGTGCACGCATC 4

RESULT 13

US-10-357-930-7957

```
; Sequence 7957, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7957
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 64, 68, 81, 83, 85, 96, 133, 147, 155, 159, 178, 190, 194,
; LOCATION: 195, 210, 222, 224, 225, 230, 242, 255, 270, 275, 281, 289,
; LOCATION: 291, 297, 309, 310, 315, 318, 324, 335, 339, 352, 353, 357,
; LOCATION: 362, 398, 400, 401, 408, 413, 420, 425, 427, 431, 434
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 439, 453, 455, 461, 466, 482, 484
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-7957

Alignment Scores:
Pred. No.: 1.98e+03 Length: 493
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-357-930-7957 (1-493)

Qy 1 IleThrArgAlaArgIle 6
| | | | | | | | | | | | | | | |
Db 98 ATTACCGTGCCCGGATA 115

RESULT 14
US-10-424-599-32616
; Sequence 32616, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
```

```
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 32616
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129457C.1
US-10-424-599-32616

Alignment Scores:
Pred. No.: 2.1e+03 Length: 524
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-424-599-32616 (1-524)

Qy 1 IleThrArgAlaArgIle 6
| | | | | | | | | | | | | | | |
Db 457 ATCACAGGAGCCAGGATA 474

RESULT 15
US-10-363-345A-10705/c
; Sequence 10705, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 10705
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 10705
US-10-363-345A-10705

Alignment Scores:
Pred. No.: 2.15e+03 Length: 537
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-363-345A-10705 (1-537)

Qy 1 IleThrArgAlaArgIle 6
| | | | | | | | | | | | | | | |
Db 298 ATAACCCGCGCAGGATA 281

RESULT 16
US-10-363-345A-10706
; Sequence 10706, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
```

; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 10706
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 10706
US-10-363-345A-10706

Alignment Scores:
Pred. No.: 2.15e+03 Length: 537
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-363-345A-10706 (1-537)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 240 ATAACCCGCGCACGAATA 257

RESULT 17

US-10-425-115-94827
; Sequence 94827, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 94827

; LENGTH: 588
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_186474C.1

US-10-425-115-94827

Alignment Scores:
Pred. No.: 2.35e+03 Length: 588
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-94827 (1-588)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 101 ATCACCCGCGCCGGATC 118

RESULT 18

US-10-437-963-18174
; Sequence 18174, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 18174
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23758C.1

US-10-437-963-18174

Alignment Scores:
Pred. No.: 2.49e+03 Length: 624
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-437-963-18174 (1-624)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 86 ATTACGCGCGCAAGATC 103

RESULT 19

US-10-027-632-23732/c
; Sequence 23732, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23732

; LENGTH: 685
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-23732

Alignment Scores:

Pred. No.: 2.72e+03 Length: 685
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-027-632-23732 (1-685)

Qy 1 IleThrArgAlaArgile 6

Db 445 ATTACAGGGCTAGATT 428

RESULT 20

US-10-027-632-23732/c

; Sequence 23732, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 10827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 23732

; LENGTH: 685

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-23732

Alignment Scores:

Pred. No.:	2.72e+03	Length:	685
Score:	27.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-10-014-101B-41 (1-6) x US-10-027-632-23732 (1-685)

Qy 1 IleThrArgAlaArgile 6

Db 445 ATTACAGGGCTAGATT 428

RESULT 21

US-10-425-114-33876

; Sequence 33876, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 33876

; LENGTH: 694

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMELMO17179H04_FLI

US-10-425-114-33876

Alignment Scores:

Pred. No.:	2.76e+03	Length:	694
Score:	27.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-10-014-101B-41 (1-6) x US-10-425-114-33876 (1-694)

Qy 1 IleThrArgAlaArgile 6

Db 262 ATAACCAGAGCAAGGATT 279

RESULT 22

US-10-425-115-35576

; Sequence 35576, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 35576

; LENGTH: 694

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_132443C.1

US-10-425-115-35576

Alignment Scores:

Pred. No.:	2.76e+03	Length:	694
Score:	27.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-014-101B-41 (1-6) x US-10-425-115-35576 (1-694)

Qy 1 IleThrArgAlaArgile 6

Db 262 ATAACCAGAGCAAGGATT 279

RESULT 23

US-10-282-122A-9537

; Sequence 9537, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21005
; LENGTH: 737
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-21005

Alignment Scores:
Pred. No.: 2.92e+03 737
Score: 27.00 6
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 17

US-10-014-101B-41 (1-6) x US-10-027-632-21005 (1-737)

Qy 1 IleThrArgAlaArgIle 6
Db 525 ATTACAAGGCGCTAGAATT 542

RESULT 27

US-10-156-761-5459/c
; Sequence 5459, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5459
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(750)
US-10-156-761-5459

Alignment Scores:
Pred. No.: 2.97e+03 750
Score: 27.00 6
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 15

US-10-014-101B-41 (1-6) x US-10-156-761-5459 (1-750)

Qy 1 IleThrArgAlaArgIle 6

Db 551 ATCACGAGGGCGAGAATC 534

RESULT 28

US-10-425-115-183342
; Sequence 183342, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 183342
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_98793C.1
US-10-425-115-183342

Alignment Scores:
Pred. No.: 2.99e+03 755
Score: 27.00 6
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 18

US-10-014-101B-41 (1-6) x US-10-425-115-183342 (1-755)

Qy 1 IleThrArgAlaArgIle 6
Db 194 ATTACACGTGCACGCATT 211

RESULT 29

US-10-425-114-15687
; Sequence 15687, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15687
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-052-F10_FLI
US-10-425-114-15687

Alignment Scores:
Pred. No.: 3.19e+03 807
Score: 27.00 6
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 17

US-10-014-101B-41 (1-6) x US-10-425-114-15687 (1-807)

Pred. No.: 3.51e+03 Length: 890
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-51212 (1-890)

Qy 1 IleThrArgAlaArgile 6
Db 70 ATTACAAGAGCTCGCATA 87

RESULT 34

US-10-437-963-100905
; Sequence 100905, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 100905
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98576C.1
US-10-437-963-100905

Alignment Scores:
Pred. No.: 3.61e+03 Length: 916
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-437-963-100905 (1-916)

Qy 1 IleThrArgAlaArgile 6
Db 809 ATAACAAGGCGCAGATT 826

RESULT 35

US-10-425-115-35581
; Sequence 35581, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 35581
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(955)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_132448C.1
US-10-425-115-35581

Alignment Scores:
Pred. No.: 3.75e+03 Length: 955
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-35581 (1-955)

Qy 1 IleThrArgAlaArgile 6
Db 826 ATCACCAGAGCAAGGATT 843

RESULT 36

US-10-437-963-63753
; Sequence 63753, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 63753
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64965C.1
US-10-437-963-63753

Alignment Scores:
Pred. No.: 3.83e+03 Length: 975
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-437-963-63753 (1-975)

Qy 1 IleThrArgAlaArgile 6
Db 62 ATAACAAGAGCTCGAATA 79

RESULT 37

US-10-425-115-65672
; Sequence 65672, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 65672
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159899C.1
US-10-425-115-65672

Alignment Scores:
Pred. No.: 3.91e+03 Length: 996
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-65672 (1-996)

QY 1 IleThrArgAlaArgile 6
|||||
Db 840 ATTACACGTGCACGCATC 857

RESULT 38

US-10-425-115-65676
; Sequence 65676, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 65676
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159901C.1
US-10-425-115-65676

Alignment Scores:
Pred. No.: 4.01e+03 Length: 1023
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-115-65676 (1-1023)

QY 1 IleThrArgAlaArgile 6
|||||
Db 854 ATTACACGTGCACGCATT 871

RESULT 39

US-10-424-599-87248/c
; Sequence 87248, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 87248
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49796C.1
US-10-424-599-87248

Alignment Scores:
Pred. No.: 4.03e+03 Length: 1027
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-424-599-87248 (1-1027)

QY 1 IleThrArgAlaArgile 6
|||||
Db 222 ATAACACGCGCGAGGATA 205

RESULT 40

US-10-425-114-32335
; Sequence 32335, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32335
; LENGTH: 1033
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73297H03_FLI
US-10-425-114-32335

Alignment Scores:
Pred. No.: 4.05e+03 Length: 1033
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-014-101B-41 (1-6) x US-10-425-114-32335 (1-1033)

QY 1 IleThrArgAlaArgile 6
|||||
Db 24 ATAACTCGCGCCCGAATC 41

Search completed: February 18, 2005, 10:15:51
Job time : 284.84 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 18, 2005, 02:20:24 ; Search time 707.52 Seconds
(without alignments)
322.797 Million cell updates/sec

Title: US-10-014-101B-41
Perfect score: 27
Sequence: 1 ITRARI 6

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10014101/runat 16022005 075846 7952/app query.fasta_1.796
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101_CGN 1 1 5453 @runat 16022005 075846 7952 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	100.0	67	9 BX536548	BX536548 Arabidops
2	27	100.0	100	2 BF174648	BF174648 MYE3555a
C 3	27	100.0	121	4 BG068639	BG068639 H3067G04 -
C 4	27	100.0	136	7 CK104188	CK104188 I018P53.5
C 5	27	100.0	140	6 CD062932	CD062932 MA1-0028U
C 6	27	100.0	152	2 AW287771	AW287771 829007E10
C 7	27	100.0	161	8 BZ637306	BZ637306 OGCBF79TC
8	27	100.0	171	8 AZ023516	AZ023516 RPCI-23-3
9	27	100.0	179	6 CB280935	CB280935 jaa05d01.

C 10	27	100.0	183	9 CC798738	CC798738 SALK_1473
C 11	27	100.0	186	6 CA485620	CA485620 WHE4321_A
12	27	100.0	194	6 CA452616	CA452616 KrlN-4_F0
13	27	100.0	195	6 CA452634	CA452634 KrlN-2_B0
14	27	100.0	214	4 BG412344	BG412344 OV2_40_G0
15	27	100.0	224	8 BH868282	BH868282 hk23h11.x
16	27	100.0	233	2 BB369534	BB369534 BB369534
C 17	27	100.0	235	2 BE764604	BE764604 PM2-NT007
18	27	100.0	237	4 BI190218	BI190218 hlf02fs.f
C 19	27	100.0	239	4 BG994575	BG994575 RC4-HT114
C 20	27	100.0	249	2 BE025443	BE025443 945028H10
21	27	100.0	253	6 CD712578	CD712578 VVB021G12
C 22	27	100.0	258	4 BM078603	BM078603 MEST122-A
23	27	100.0	259	1 AV323709	AV323709 AV323709
24	27	100.0	260	2 AW620066	AW620066 819 MARC
C 25	27	100.0	261	4 BI055989	BI055989 PM2-GN043
26	27	100.0	261	6 CA811112	CA811112 CA22LI041
27	27	100.0	262	2 BB319596	BB319596 BB319596
28	27	100.0	263	8 B81555	B81555 CIT-HSP-206
C 29	27	100.0	265	7 CR516082	CR516082 CR516082
30	27	100.0	266	2 BE529872	BE529872 M75N15STM
C 31	27	100.0	266	7 CK691445	CK691445 ZF101-P00
32	27	100.0	267	2 BB577396	BB577396 BB577396
C 33	27	100.0	267	8 BZ671989	BZ671989 PUBKV67TD
34	27	100.0	269	8 BH228153	BH228153 1006144E1
C 35	27	100.0	279	6 CB921222	CB921222 VVD068E05
36	27	100.0	285	6 CD152034	CD152034 ML1-0027T
37	27	100.0	286	2 AW870159	AW870159 NXNV_124
38	27	100.0	287	2 BB336254	BB336254 BB336254
39	27	100.0	288	6 CD061127	CD061127 MA1-0016U
C 40	27	100.0	289	4 BM348722	BM348722 MEST299-G
C 41	27	100.0	290	9 BX198253	BX198253 Danio rer
C 42	27	100.0	293	4 BM349587	BM349587 MEST252-B
C 43	27	100.0	295	2 BE580170	BE580170 kq38a03.y
C 44	27	100.0	296	1 AU023430	AU023430 AU023430
45	27	100.0	297	6 CB339189	CB339189 CA23EI03I

ALIGNMENTS

RESULT 1
BX536548/c
LOCUS BX536548 67 bp DNA linear GSS 04-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-528G02-020333,
genomic survey sequence.

ACCESSION BX536548
VERSION BX536548.1 GI:31413678
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829
PUBMED 12874060

REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147
PUBMED 14756321

REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 67)
Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
F9K20. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
1..67
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-528G02-020333"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Alignment Scores:
Pred. No.: 1.51e+03 Length: 67
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-41 (1-6) x BX536548 (1-67)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 26 ATAACACGAGCCAGAATT 9

RESULT 2
BF174648
LOCUS
DEFINITION MYE3555a Myeloma (MYE) CDNA library Homo sapiens cDNA, mRNA
sequence.
BF174648
BF174648.1 GI:13440862
EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
AUTHORS Claudio,J.O., Masih-Khan,E., Tang,H., Goncalves,J., Voralia,M.,
Li,Z.H., Nadeem,V., Cukerman,E., Francisco-Pabalan,O., Liew,C.C.,
Woodgett,J.R. and Stewart,A.K.
TITLE A molecular compendium of genes expressed in multiple myeloma
JOURNAL Blood 100 (6), 2175-2186 (2002)
MEDLINE 22188429
PUBMED 12200383
COMMENT Contact: A. Keith Stewart, M.D.
Oncology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639

us-10-014-101b-41.rst

Fax: (416) 946-6546
Email: k.stewart@utoronto.ca
PCR Primers
FORWARD: 5'-GCCAAGCTCGAATTAAACCCCTCACTAAAGG-3'
BACKWARD: 5'-CCAGTGAATTGTATACGACTCACTATAGGCG-3'
Seq primer: 5'-GAAATTAACCCCTCACTAAAGG-3'.

FEATURES
source
Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="male"
/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="multiple myeloma"
/clone_lib="Myeloma (MYE) CDNA library"
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
XhoI; Myeloma cells from multiple myeloma patients' bone
marrow were purified by magnetic cell sorting. mRNA were
purified and an oligo d(T)18 primer containing XhoI
restriction site was used to prime first strand synthesis
using M-MLV reverse transcriptase. To protect the cDNAs
from XhoI digestion in subsequent cloning step, the
nucleotide analogue 5-methyl-dCTP was added to the
nucleotide mixture and [a-32P]dATP was added to monitor
the quantity and quality of first strand synthesis. After
second-strand synthesis and blunting of cDNA termini,
EcoRI adapters were ligated, followed by kinase treatment
and digestion with XhoI. The cDNAs were then
size-fractionated using Sephacryl S-500 column and then
ligated into EcoRI and XhoI digested Lambda Zap Express
vector. The ligation product was packaged using Gigapack
II packaging extract. The library had primary titre of
approx. 1x10⁶. Clones from the primary library were
randomly selected for single pass sequencing."

ORIGIN
Alignment Scores:
Pred. No.: 2.24e+03 Length: 100
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x BF174648 (1-100)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 65 ATAACGCGAGCGAGATC 82

RESULT 3
BG068639/c
LOCUS
DEFINITION H3067G04-3 NIA Mouse 15K CDNA Clone Set Mus musculus cDNA clone
H3067G04 3', mRNA sequence.
ACCESSION BG068639
VERSION BG068639.2 GI:40016430
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 121)
AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
TITLE Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
MEDLINE 20381348
PUBMED 10922068
COMMENT On Jan 26, 2001 this sequence version replaced gi:12551208.

Other_ESTs: H3067G04-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://igsun.grc.nia.nih.gov/cdna/15k.html> for details.
Plate: H3067 row: G column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 121
POLYA=Yes.

FEATURES

source
1. 121
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:H3067G04-3"
/db_xref="taxon:10090"
/clone="H3067G04"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA libraries"
libraries"
/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Alignment Scores:
Pred. No.: 2.7e+03 Length: 121
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x BG068639 (1-121)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 25 ATCAAGAGAGCCAGGATT 8

RESULT 4

CK104188/c
LOCUS CK104188 136 bp mRNA linear EST 01-DEC-2003
DEFINITION I018P53.5PR Populus senescing leaves cDNA library Populus tremula
CDNA clone I018P53 5', mRNA sequence.
ACCESSION CK104188
VERSION CK104188.1 GI:38588513
KEYWORDS EST.
SOURCE Populus tremula
ORGANISM Populus tremula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE

AUTHORS
1 (bases 1 to 136)
Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,
Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,
Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.
A Populus EST resource for functional genomics
Unpublished (2003)

TITLE

JOURNAL I018P53P, I018P53.3PR

COMMENT

Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
Umea University
901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plantphys.umu.se.

FEATURES

source

1. 136
/organism="Populus tremula"
/mol_type="mRNA"
/db_xref="taxon:113636"
/clone="I018P53"
/tissue_type="Senescing leaves"
/clone_lib="Populus senescing leaves cDNA library"

ORIGIN

Alignment Scores:
Pred. No.: 3.03e+03 Length: 136
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-41 (1-6) x CK104188 (1-136)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 109 ATCACCAGGCACGCATT 92

RESULT 5

CD062932/c

LOCUS

CD062932 140 bp mRNA linear EST 14-SEP-2003
DEFINITION MA1-0028U-A010-D07-U.B MA1-0028 Schistosoma mansoni cDNA clone
MA1-0028U-A010-D07.B, mRNA sequence.
ACCESSION CD062932
VERSION CD062932.1 GI:34614092
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni

REFERENCE

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 140)

AUTHORS

Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni

TITLE

JOURNAL Nat. Genet. 35 (2), 148-157 (2003)

MEDLINE

22879926

PUBMED

12973350

COMMENT

Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquímica

Instituto de Química - Universidade de São Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL <http://bioinfo.iq.usp.br/schisto/>
Plate: MA1-0028U-A010 row: 7 column: D.

FEATURES

Location/Qualifiers
1. .140
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MA1-0028U-A010-D07.B"
/sex="mixed pool"
/dev_stage="adult"
/lab_host="Mesocricetus auratus"
/clone_lib="MA1-0028"
/note="Vector: SureClone"

ORIGIN

Alignment Scores: 3.12e+03 Length: 140
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-014-101B-41 (1-6) x CD062932 (1-140)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 29 ATCACTCGTGCACGCATT 12

RESULT 6

AW287771/c 152 bp mRNA linear EST 09-FEB-2000
LOCUS 829007E10.x1 829 - Silk infected with Fusarium Zea mays cDNA, mRNA
DEFINITION sequence.

ACCESSION AW287771 GI:6681784
VERSION AW287771.1
KEYWORDS EST.

SOURCE

Ze mays
Ze mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 152)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 829007 row: E column: 10.

FEATURES

source
Location/Qualifiers
1. .152
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="silk"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="829 - Silk infected with Fusarium"
/note="Organ: silk; Vector: pBluescript II XR; Site 1:
XhoI; Site 2: EcoRI; cDNA library of silks infected with 1
microliter of 500,000 spores/ml solution of Fusarium
graminearum DAOM 180378. Prepared by Sharon Allard of

ORIGIN

Alignment Scores: 3.38e+03 Length: 152
Pred. No.: 27.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 2

US-10-014-101B-41 (1-6) x AW287771 (1-152)

Qy 1 IleThrArgAlaArgIle 6
|||||
Db 90 ATTACAGTGCACGCATT 73

RESULT 7

BZ637306/c 161 bp DNA linear GSS 29-JAN-2003
LOCUS OGCBF79TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMEMa0132N14,
DEFINITION genomic survey sequence.

ACCESSION BZ637306 GI:28088139
VERSION BZ637306.1
KEYWORDS GSS.

SOURCE

Ze mays
Ze mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

TITLE

JOURNAL Consortium for Maize Genomics

COMMENT

Other GSSs: OGCBF79TM
Unpublished (2002)

Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

FEATURES

source
1. .161
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMEMa0132N14"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.: 3.58e+03 Length: 161
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x BZ637306 (1-161)

Qy 1 IleThrArgAlaArgIle 6

|||||

Db 35 ATACAGGCGCAAGGATT 18

```
RESULT 8
AZ023516
LOCUS
DEFINITION
  RPCI-23-336P9.TV RPCI-23 Mus musculus genomic clone RPCI-23-336P9,
  genomic survey sequence.
ACCESSION
VERSION
  AZ023516
KEYWORDS
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 171)
AUTHORS
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
  Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
  Jong,P. and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other GSSs: RPCI-23-336P9.TJ
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (info@resgen.com). BAC end page:
  http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
  Plate: 336 row: P column: 9
  Seq primer: T7
  Class: BAC ends.
FEATURES
  source
    location/Qualifiers
      1..171
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="RPCI-23-336P9"
        /sex="Female"
        /lab_host="DH10B"
        /clone_lib="RPCI-23"
        /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
        EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
        brain genomic DNA was isolated and partially digested
        with a combination of EcoRI and EcoRI Methylase. Size
        selected DNA was cloned into the pBACe3.6 vector at the
        EcoRI sites. The ligation products were transformed into
        DH10B electrocompetent cells (BRL Life Technologies). "
```

```
ACCESSION
VERSION
  CB280935
KEYWORDS
SOURCE
  Anolis sagrei (brown anole)
ORGANISM
  Anolis sagrei
REFERENCE
  1 (bases 1 to 179)
AUTHORS
  Losos,J., Gibson-Brown,J., Sanger,T.J., Langwith,S., Murphy,C.,
  Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
  Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E.,
  Bennett,J., Ronko,I., Tsagareishvili,R., Maguire,L., Kennedy,S.,
  Waterston,R. and Wilson,R.
  Packard/Washington University Lizard Limb Bud EST Project
  Unpublished (2003)
  Contact: Jeremy Gibson-Brown
  Packard/Washington University Lizard Limb Bud EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Library was constructed by Jeremy Gibson-Brown DNA sequencing by:
  Washington University Genome Sequencing Center For information on
  obtaining a clone please contact: Jeremy Gibson-Brown
  (gibbro@biology.wustl.edu)
  Putative full length read
  vector to vector length is
  Seq primer: T7.
FEATURES
  source
    Location/Qualifiers
      1..179
        /organism="Anolis sagrei"
        /mol_type="mRNA"
        /db_xref="taxon:38937"
        /lab_host="DH10B"
        /clone_lib="Anolis sagrei limb bud 1"
        /note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2:
        BamHI; 1st strand primed with an oligo (dT) primer: double
        stranded cDNA was cloned into the EcoRI and BamHI sites of
        the pBluescript SK+ vector. Primary library;
        non-amplified."
ORIGIN
Alignment Scores:
Pred. No.:      3.97e+03      Length:      179
Score:          27.00        Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    100.00%      Indels:      0
DB:              6           Gaps:       0
US-10-014-101B-41 (1-6) x CB280935 (1-179)
Qy      1 IleThrArgAlaArgIle 6
        |||||
Db      24 ATCACCAGAGAGCCAGAATA 41
RESULT 10
CC798738/c
LOCUS
DEFINITION
  CC798738
  SALK_147359.37.35.n Arabidopsis thaliana TDNA insertion lines
  Arabidopsis thaliana genomic clone SALK_147359.37.35.n, genomic
  survey sequence.
ACCESSION
VERSION
  CC798738
KEYWORDS
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  1 (bases 1 to 183)
REFERENCE
  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
```

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

JOURNAL COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g21390.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..183
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_147359.37.35.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Alignment Scores:
Pred. No.: 4.06e+03 Length: 183
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-014-101B-41 (1-6) x CC798738 (1-183)

Qy 1 IleThrArgAlaArgIle 6

|||||

Db 72 ATAACAAGAGCTCGGATT 55

RESULT 11

CA485620/c

LOCUS

DEFINITION WHE4321_A02_A03ZS Wheat meiotic anther cDNA library EST 14-NOV-2002
aestivum cDNA clone WHE4321_A02_A03, mRNA sequence.

ACCESSION CA485620

VERSION CA485620.1

KEYWORDS EST. GI:24979625

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 186)

Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R.,

Pham,J., Rausch,C.J., Sutton,T., Woo,J. and Wilson,C.

The structure and function of the expressed portion of the wheat

genomes - Meiotic anther cDNA library

Unpublished (2002)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanders@pw.usda.gov

Sequences have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

FEATURES

source

Seq primer: SK primer.

Location/Qualifiers

1..186

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE4321_A02_A03"

/dev_stage="Meiotic stages pre-meiosis-metaphase I"

/lab_host="E. coli DH10B"

/clone_lib="Wheat meiotic anther cDNA library"

/note="Vector: pSPORT1; Site 1: Sali; Site 2: NotI; Plants
were grown in a glasshouse. Anther meiotic stage was
determined by removing anthers from individual primary
florets. One anther was sacrificed for microscopic
staging, and if determined to be between (and including)
meiotic stages pre-meiosis and metaphase I, the remaining
two anthers were collected and pooled for library
construction. The tissue, total RNA, and poly(A) RNA were
prepared, cDNA synthesised, and directionally ligated into
pSPORT1 by Tim Sutton in the P Langridge Lab at the
Department of Plant Science, University of Adelaide, Waite
Campus, Australia. Average insert size 1.5Kb. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

ORIGIN

Alignment Scores:
Pred. No.: 4.12e+03 Length: 186
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CA485620 (1-186)

Qy 1 IleThrArgAlaArgIle 6

|||||

Db 79 ATCACTCGCGCAAGAATC 62

RESULT 12

CA452616

LOCUS

DEFINITION KrIN-4_F01 subtracted cDNA library of maize inbred line
H95-Rp1-Kr1N Zea mays cDNA clone KrIN-4_F01, mRNA sequence.

ACCESSION CA452616

VERSION CA452616.1

KEYWORDS EST. GI:24934398

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 194)

Bai,J., Fellers,J.P., Leach,J.E. and Hulbert,S.H.

Comparison of pathogen induced defense gene profiles on maize lines

with different resistance genes

Unpublished (2003)

Contact: Bai J

Department of Plant Pathology

Kansas State University

4024 Throckmorton Plant Sciences Center, Manhattan, KS 66506, USA

Tel: 785-532-2328

Fax: 785-532-5692

Email: jianfa@plantpath.ksu.edu

Seq primer: T7.

FEATURES

source

Location/Qualifiers

1..194

/organism="Zea mays"

/mol_type="mRNA"

/strain="inbred line H95-Rp1-Kr1N"

/db_xref="taxon:4577"
/clone="KrlN-4_F01"
/tissue_type="Spontaneously lesioned leaves"
/dev_stage="4 week-old plants"
/clone_lib="subtracted cDNA library of maize inbred line
H95-Rp1-KrlN"
/note="Vector: pUC19; Supression subtractive
hybridization; cloned into pUC19 vector. From a subtracted
cDNA library of maize inbred line H95 carrying the
Rpl-KrlN gene that conditions defense response phenotype."

ORIGIN

Alignment Scores:
Pred. No.: 4.3e+03 Length: 194
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CA452616 (1-194)

Qy 1 IleThrArgAlaArgile 6

Db 170 ATTACACGTGCACGCATC 187

RESULT 13

CA452634

LOCUS

DEFINITION

KrlN-2 B09 subtracted cDNA library of maize inbred line

H95-Rp1-KrlN Zea mays cDNA clone KrlN-2_B09, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 195)

Bai,J., Fellers,J.P., Leach,J.E. and Hulbert,S.H.

Comparison of pathogen induced defense gene profiles on maize lines

with different resistance genes

Unpublished (2003)

Contact: Bai J

Department of Plant Pathology

Kansas State University

4024 Throckmorton Plant Sciences Center, Manhattan, KS 66506, USA

Tel: 785-532-2328

Fax: 785-532-5692

Email: jianfa@plantpath.ksu.edu

Seq primer: T7.

FEATURES

source

1. .195

/organism="Zea mays"

/mol_type="mRNA"

/strain="inbred line H95-Rp1-KrlN"

/db_xref="taxon:4577"

/clone="KrlN-2_B09"

/tissue_type="Spontaneously lesioned leaves"

/dev_stage="4 week-old plants"

/clone_lib="subtracted cDNA library of maize inbred line

H95-Rp1-KrlN"

/note="Vector: pUC19; Supression subtractive

hybridization; cloned into pUC19 vector. From a subtracted

cDNA library of maize inbred line H95 carrying the

Rpl-KrlN gene that conditions defense response phenotype."

ORIGIN

Alignment Scores:

Pred. No.: 4.32e+03 Length: 195

Score: 27.00 Matches: 6

Percent Similarity: 100.00% Conservatve: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CA452634 (1-195)

Qy 1 IleThrArgAlaArgile 6

Db 171 ATTACACGTGCACGCATC 188

RESULT 14

BG412344

LOCUS

DEFINITION

OV2_40_G07.b1_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 214)

Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and

Pratt,L.H.

An EST database from Sorghum: ovaries of varying immature stages

Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Seq primer: JEN REV

High quality sequence stop: 33

POLYA=No.

FEATURES

source

1. .214

/organism="Sorghum bicolor"

/mol_type="mRNA"

/db_xref="taxon:4558"

/clone_lib="Ovary 2 (OV2)"

/note="Organ: Mix of ovaries of varying immature stages

from 8-week-old plants; Vector: pBluescript II from Lambda

Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made

from poly-A RNA in the cloning vector lambda ZAP II.

Clones to be sequenced were prepared by mass excision."

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+03 Length: 214

Score: 27.00 Matches: 6

Percent Similarity: 100.00% Conservatve: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x BG412344 (1-214)

Qy 1 IleThrArgAlaArgile 6

Db 149 ATCACCCTGCCAGGATT 166

RESULT 15

BH868282

LOCUS

DEFINITION

hk23hl1.x7 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays

genomic clone hk23hl1 5', genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

BH868282 224 bp DNA linear GSS 05-AUG-2002

SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 224)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hk23 row: h column: 11
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 224.
Location/Qualifiers
1..224
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hk23h11"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mpl9, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."
ORIGIN
Alignment Scores:
Pred. No.: 4.95e+03 Length: 224
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-014-101B-41 (1-6) x BH868282 (1-224)
QY 1 IleThrArgAlaArgIle 6
|||||
Db .188 ATAACCGGGCCAGGATC 205
RESULT 16
BB369534
LOCUS
DEFINITION BB369534 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130048M07 3', mRNA sequence.
ACCESSION BB369534
VERSION BB369534.1 GI:9081363
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 233)
REFERENCE
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Hayatsu,N., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,

TITLE
JOURNAL
COMMENT
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Location/Qualifiers
1..233
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C130048M07"
/sex="mixed"
/tissue type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 16 days embryo head"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTITTTTITTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+03 Length: 233
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-014-101B-41 (1-6) x BB369534 (1-233)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 34 ATTACAAGAGCCCGTATC 51

RESULT 17
BE764604/c

LOCUS BE764604 235 bp mRNA linear EST 19-SEP-2000
DEFINITION PM2-NT0075-150500-002-b01 NT0075 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE764604
VERSION BE764604.1 GI:10194528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 235)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM2-NT0075-150500-002-b01&t3=2000-05-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence stop: 151.
FEATURES
Location/Qualifiers
1..235
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0075"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 5.19e+03 Length: 235
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x BE764604 (1-235)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 108 ATCACCAGGCCCGGATC 91

RESULT 18
BI190218

LOCUS BI190218 237 bp mRNA linear EST 10-JUL-2001
DEFINITION hlf02fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone hlf02fs 3', mRNA sequence.
ACCESSION BI190218
VERSION BI190218.1 GI:14663897
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
AUTHORS 1 (bases 1 to 237)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 71 1.3 gi|323156|pir||S3215 protein-tyrosine kinase (EC 2.7.1.112) GCT
Seq primer: M13-20
High quality sequence stop: 79.
FEATURES
Location/Qualifiers
1..237
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="hlf02fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"

ORIGIN
Alignment Scores:
Pred. No.: 5.23e+03 Length: 237
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x BI190218 (1-237)

Qy 1 IleThrArgAlaArgile 6
|||||
Db 191 ATAACAAGAGCTCGAATC 208

RESULT 19
BG994575/c

LOCUS BG994575 239 bp mRNA linear EST 13-JUN-2001
DEFINITION RC4-HT1141-130201-011-d06 HT1141 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG994575
VERSION BG994575.1 GI:14398645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 239)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC4&t2=RC4-HT1141-130201-011-d06&t3=2001-02-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 108
High quality sequence stop: 159.

FEATURES

source

1. .239
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1141"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 5.27e+03 Length: 239
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101b-41 (1-6) x BG994575 (1-239)

Qy 1 IleThrArgAlaArgIle 6

Db 207 ATTACCGGGCCCGTATA 190

RESULT 20

BE025443/c

LOCUS

DEFINITION 945028H10.y2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.

ACCESSION BE025443

VERSION BE025443.1 GI:8318803

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 249)

Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

JOURNAL

COMMENT

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945028 row: H column: 10.

FEATURES

source

1. .249
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W23"
/db_xref="taxon:4577"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site 1: EcoRI; CDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."

ORIGIN

Alignment Scores:
Pred. No.: 5.49e+03 Length: 249
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101b-41 (1-6) x BE025443 (1-249)

Qy 1 IleThrArgAlaArgIle 6

Db 50 ATTACACGTGCACGCATT 33

RESULT 21

CD712578

LOCUS

DEFINITION CD712578 253 bp mRNA linear EST 25-JUN-2003
VVB021G12 403503 An expressed sequence tag database for abiotic
stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
cDNA clone VVB021G12 5, mRNA sequence.

ACCESSION CD712578

VERSION CD712578.1 GI:32246759

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

1 (bases 1 to 253)

Cramer,G.R. and Cushman,J.C.

An expressed sequence tag database for abiotic stressed leaves of
Vitis vinifera var. Chardonnay

Unpublished (2002)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer (backward)

Plate: 0 row: G column: 12

Seq primer: T7 20mer (forward)

High quality sequence stop: 253.

FEATURES
source

Location/Qualifiers
1. .253
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVB021G12"
/tissue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 5.58e+03 Length: 253
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CD712578 (1-253)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 143 ATTACAAGACGACGGATA 160

RESULT 22

BM078603/c

LOCUS

DEFINITION
MEST122-A01.T3 ISUM4-TN Zea mays cDNA clone MEST122-A01 3', mRNA

ACCESSION

VERSION
BM078603.1 GI:16925535

KEYWORDS

SOURCE
Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS
Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.

TITLE

Expressed Sequence Tags from B73 Maize Seedlings and Silks

JOURNAL

COMMENT
Unpublished (2001)

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

Phred software.

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b

rt>). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.tigr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR Primers

FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA

CTA TAG)

BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC

TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES

source

Location/Qualifiers

1. .258

/organism="Zea mays"

/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST122-A01"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/clone_lib="ISUM4-TN"
/note="Vector: pT73PAC; Site 1: EcoRI; Site 2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI Oligo-dT primer (5'
AACTGGAAGAATTGCGGCGCAGGAATTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

ORIGIN

Alignment Scores:
Pred. No.: 5.69e+03 Length: 258
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-014-101B-41 (1-6) x BM078603 (1-258)

QY 1 IleThrArgAlaArgIle 6
|||||
Db 143 ATTACACGTGCACGCATT 126

RESULT 23

AV323709

LOCUS

DEFINITION

AV323709 RIKEN full-length enriched, 11 days embryo head Mus
musculus cDNA clone 6230412A13 3' similar to D10916 Mouse mRNA of
NEDD-6 gene, 3'terminal sequence, mRNA, mRNA sequence.

ACCESSION

VERSION
AV323709.1 GI:6293626

KEYWORDS

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 259)

REFERENCE

AUTHORS

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,

Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and

Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1..259
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6230412A13"
/sex="mixed"
/tissue_type="head"
/dev_stage="11 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 11 days embryo head"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCTCGAGTTAATTAATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN

Alignment Scores:
Pred. No.: 5.71e+03 Length: 259
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-014-101B-41 (1-6) x AV323709 (1-259)

QY 1 IleThrArgAlaArgile 6
|||||
Db 14 ATCACACGGCCCGAATC 31

RESULT 24

AW620066

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 260)

AUTHORS

Smith,T.P.L., Fahrenkrug,S.C., Rohrer,G.A., Simmen,F.A.,

Rexroad,C.E. and Keele,J.W.
Mapping of expressed sequence tags from a porcine early embryonic cDNA library
Anim. Genet. 32 (2), 66-72 (2001)
21314990
11421940
Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: GGAAACAGCTATGACCATG
BACKWARD: GTAAACGACGGCCAGT
Seq primer: AATTAACCTCACTAAAGGG.

FEATURES

source

Location/Qualifiers
1..260
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="Day 12 whole embryos"
/lab_host="XL0LR"
/clone_lib="MARC PBE"
/note="Vector: pBLUESCRIPT SK-; Site 1: EcoRI; Site 2: XhoI; Library made from pool of embryos in spherical and filamentous stages of development (7.5% and 92.5%, respectively, of each stage) as described in Choi et al, Endocrinology 137, 1457-67, 1996."

ORIGIN

Alignment Scores:
Pred. No.: 5.73e+03 Length: 260
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x AW620066 (1-260)

QY 1 IleThrArgAlaArgile 6
|||||
Db 153 ATTACAAGGCCAGATC 170

RESULT 25

BI055989/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 261)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

PUBMED

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil.
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM2&t2=PM2-GN0431-150201-001-c03&t3=2001-02-15&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 261.

FEATURES

Source

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0431"
/note="Organ: placenta normal; Vector: puc18; Site 1:
SmaI; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

```

ORIGIN

Alignment Scores:		
Pred. No.:	5.75e+03	261
Score:	27.00	6
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	100.00%	0
DE:	4	0
Length:		
Matches:		
Conservative:		
Mismatches:		
Indels:		
Gaps:		

US-10-014-101B-41 (1-6) x BI055989 (1-261)

Qy

1 IleThrArgAlaArgIle 6
↑↑↑↑↑↑↑↑↑↑↑↑↑↑↑↑
Db

228 ATAACCCGGGCCGTATA 211

RESULT 26				
CA811112				
LOCUS	CA811112	261 bp	mRNA	linear EST 10-APR-2003
DEFINITION	CA22LI04IR-D10 Cabernet Sauvignon Leaf - CA22LI Vitis vinifera cDNA clone CA22LI04IR-D10 3', mRNA sequence.			

SOURCE	ORGANISM
Vitis vinifera	Vitis vinifera
Vitis vinifera	Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.	rosids; Vitaceae; Vitis.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 261)	Goes da Silva, F., Lim, H., Iandolino, A., Baek, J., Leslie, A., Xu, J., Jones, K., Walker, M. A. and Cook, D. R.	Transcriptional responses of <i>Vitis vinifera</i> to infection by the bacterial pathogen <i>Xylella fastidiosa</i>

CAES Genome Facility
UC Davis Department of Plant Pathology
1 Shields Ave., Davis, CA 95616, USA
Tel: 530 754 6561

FEATURES

Source

/organism="Vitis vinifera"

```

/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CA22LI04IR-D10"
/sex="hermaphrodite"
/dev_stage="late season sample"
/lab_host="DH5alpha"
/clone_lib="Cabernet Sauvignon Leaf - CA22LI"
/notes="Organ: Leaf; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CA22LI is a cDNA library of Cabernet Sauvignon leaves. The leaves were collected on September 20, 2001, in Napa Valley, California, and represent leaves in late season development. These leaves were verified to be infected with the bacterial pathogen, Xylella fastidiosa, based on a diagnostic assay using PCR and Xylella-specific primer pairs. Plants were symptomatic at the time of collection. cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5' -AAGCAGTGGTATCAACGCAGAGTGGCCATTACGCGCGG-3', and 5' -ATTCTAGAGCGGAGGCGGCGCATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

```

ORIGIN

Alignment Scores:	
Pred. No.:	5.75e+03
Score:	27.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
Length:	261
Matches:	6
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-014-101B-41 (1-6) x CA811112 (1-261)

Qy 1 IleThrArgAlaArgile 6

RESULT 27
BB319596

LOCUS	BB19596	262 bp	mRNA	linear	EST 11-JUL-2000
DEFINITION	BB19596 RIKEN full-length enriched, adult male corpora quadrigemina <i>Mus musculus</i> cDNA clone B230381C22 3', mRNA sequence.				

ACCESSION BB319596

VERSION BB319596.1 GI:9026631

KEYWORDS EST.

SOURCE *Mus musculus* (house mouse)

ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 262)

REFERENCE

AUTHORS

TITLE RIKEN Mousse ESTs (Konno, H., et al.)

JOURNAL Unpublished (2000)

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Ja
tel: 81-45-503-9222

Mouse ArrayTAG cDNA
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=462 Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.

FEATURES
source

Location/Qualifiers
1..265
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONP462C06364"
/lab_host="DH10B"
/clone_lib="Mouse pBluescript Lion"

ORIGIN

Alignment Scores:
Pred. No.: 5.84e+03 Length: 265
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-014-101B-41 (1-6) x CR516082 (1-265)

QY 1 IleThrArgAlaArgile 6
|||||
Db 159 ATAACAAGGCCCGCATC 142

RESULT 30

BE529872
LOCUS BE529872 266 bp mRNA linear EST 19-MAR-2001
DEFINITION M75N15STM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone 600039263R1 5', mRNA sequence.

ACCESSION BE529872
VERSION BE529872.1 GI:9787850

KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
TITLE A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
MEDLINE 20567808
PUBMED 11115876

COMMENT

Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI
48824, USA
Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.

FEATURES

source

1..266
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"

/db_xref="taxon:3702"
/clone="600039263R1"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"

ORIGIN

Alignment Scores:
Pred. No.: 5.86e+03 Length: 266
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x BE529872 (1-266)

QY 1 IleThrArgAlaArgile 6
|||||
Db 226 ATCACTCGGCACGAATC 243

RESULT 31

CK691445/c

LOCUS CK691445

DEFINITION CK691445 266 bp mRNA linear EST 30-MAR-2004

IMAGE:7155314 5', mRNA sequence.

ACCESSION CK691445.1 GI:42443781

VERSION CK691445

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 266)

REFERENCE

AUTHORS Wei,C., Mathavan,S., Thoreau,H., Lim,L., Lee,C. and Ruan,Y.

TITLE Genome Institute of Singapore, Zebrafish Gene Collection

JOURNAL Unpublished (2004)

COMMENT Contact: Ruan Y

Cloning and Sequencing

Genome Institute of Singapore

60 Biopolis Street, #02-01, Genome, Singapore 138672

Tel: +65 6478 8073

Fax: +65 6478 9059

Email: ruanyj@gis.a-star.edu.sg

GIS Clone ID: ZF101-P00056-BR2_G24

PCR Primers

FORWARD: M13

BACKWARD: M13

Plate: ZF101-P00056-BR2 row: G column: 24

Seq primer: CCGCATAACTTGATAGCA

High quality sequence stop: 266.

FEATURES

source

1..266
/organism="Danio rerio"
/mol_type="mRNA"
/strain="Singapore local strain"
/db_xref="taxon:7955"
/clone="IMAGE:7155314"
/tissue_type="Embryo"
/dev_stage="7 Different embryonic Stages(From just
fertilized Embryos to 72 hours just hatched baby fish)"
/lab_host="DH10B"
/clone_lib="GISF001 ra"

/note="Vector: pDNR-LIB; Site_1: Sfi A (GGCATTACGGCC);
Site_2: Sfi B (GGCGAGCGGCC); Priming method: Sfi-(dt)30
Primed ; Priming sequence:
5.ATTCTAGAGCGCGCGCGGCACATG(T)30VN ; Directionally
cloned, 5' cloning site: Sfi A site GGCATTACGGCC ; 5'
linker/adaptor sequence: 5.AAGCAGTGGTATCAACGACAGTGGCC ;

3' cloning site: Sfi B site GGCCGAGCGGCC ; 3' linker/adaptor sequence: same as the priming sequence ; Average insert size: 2kb ; For PCR insert analysis: Use M13 Forward and reverse primers ; Library Amplified ; Recombinants (inserts): 98% ; Library complexity: 5x10⁶ ; Full-length construction (method): SMART, a Clontech method The pooled tissue RNA was collected and used to construct full length enriched cDNA library and also served as template to synthesize complex first strand cDNA probe. Two high density colony arrays were made from over 110K cDNA clones and hybridized with the probes. Low intensity clones were selected as they represented rare expressed clones. The hybridization intensities for all clones span from 0 to 1.8 million counts and the low abundant class ranged from 0 to 13,000."

ORIGIN

Alignment Scores: Pred. No.: 5.86e+03 Length: 266 Score: 27.00 Matches: 6 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 7 Gaps: 0

US-10-014-101B-41 (1-6) x CK691445 (1-266)

QY 1 IleThrArgAlaArgIle 6
|||||

Db 89 ATACACGAGCGAGAATC 72

RESULT 32

BB577396

LOCUS

BB577396 RIKEN full-length enriched, 11 days embryo head Mus
musculus cDNA clone 6230401E23 5', mRNA sequence.

BB577396

BB577396.1 GI:11473940

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Alignment Scores: Pred. No.: 5.88e+03 Length: 267 Score: 27.00 Matches: 6 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 2 Gaps: 0

US-10-014-101B-41 (1-6) x BB577396 (1-267)

QY 1 IleThrArgAlaArgIle 6
|||||

Db 144 ATTACCAGAGCAAGAATC 161

TITLE

JOURNAL

COMMENT

RESULT 33

BZ671989/c

LOCUS

DEFINITION BZ671989 PUBKV67TD ZM_0.6 1.0 KB Zea mays genomic clone ZMMBta078K14, genomic survey sequence.

ACCESSION BZ671989

VERSION BZ671989.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 267)

AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.

TITLE Maize Genomics Consortium

JOURNAL Unpublished (2003)

COMMENT Contact: Cathy Whitelaw

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..267

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="6230401E23"

/sex="mixed"

/tissue_type="head"

/dev_stage="11 days embryo"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 11 days embryo head"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source

Location/Qualifiers
1. .267
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa078K14"
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Alignment Scores:
Pred. No.: 5.88e+03 Length: 267
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x BZ671989 (1-267)

Qy 1 IleThrArgAlaArgIle 6
Db 254 ATCAACAGGGCAGGTATC 237

RESULT 34

BH228153

LOCUS BH228153 269 bp DNA linear GSS 08-NOV-2001
DEFINITION 1006144E12.xl1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION BH228153

VERSION BH228153.1 GI:16828887

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 269)

walbot,v.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

JOURNAL

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006144 row: 5

Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1. .269
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

/clone_lib="1006 - RescueMu Grid G"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site_1: BamHI; Site_2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Alignment Scores:
Pred. No.: 5.92e+03 Length: 269
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101B-41 (1-6) x BH228153 (1-269)

Qy 1 IleThrArgAlaArgIle 6

Db 161 ATAACGCGCCCGAATC 178

RESULT 35

CB921222/c

LOCUS CB921222

DEFINITION CB921222.1 GI:30135884

stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera

CDNA clone VVD068E05 5, mRNA sequence.

ACCESSION CB921222

VERSION CB921222.1 GI:30135884

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

1 (bases 1 to 279)

Cushman,J.C.

An expressed sequence tag database for abiotic stressed berries of

Vitis vinifera var. Chardonnay

Unpublished (2002)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer (backward)

Plate: 068 row: E column: 05

Seq primer: T3 20mer

High quality sequence stop: 279.

Location/Qualifiers

1. .279

/organism="Vitis vinifera"

/mol_type="mRNA"

/db_xref="taxon:29760"

/clone="VVD068E05"

/tissue_type="berries"

/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"

/clone_lib="An expressed sequence tag database for abiotic

stressed berries of Vitis vinifera var. Chardonnay"

/note="Vector: Lambda Uni-zap XR, Bluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

ECORI; Site_2: XhoI"

Alignment Scores:

Pred. No.: 6.14e+03 Length: 279

Score: 27.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CB921222 (1-279)

QY 1 IleThrArgAlaArgIle 6
Db 95 ATTACAAGACGCGGATA 78

RESULT 36

CD152034

LOCUS

DEFINITION

ML1-0027T-D047-H07-U.G ML1-0027 Schistosoma mansoni CDNA clone

ML1-0027T-D047-H07.G, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 285)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,

Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,

Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,

Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,

Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,

Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,

Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,

Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,

Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acoelomate human parasite Schistosoma

mansoni

Nat. Genet. 35 (2), 148-157 (2003)

22879926

12973350

Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquimica

Instituto de Quimica - Universidade de Sao Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjo@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST

Genome Project. All sequences in the project were assembled and

annotated. This entry and all the assembled sequences can be seen

in the following URL http://bioinfo.iq.usp.br/schisto/

Plate: ML1-0027T-D047 row: 7 column: H.

Location/Qualifiers

1. .285

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="ML1-0027T-D047-H07.G"

/sex="mixed pool"

/dev_stage="miracidium"

/clone_lib="ML1-0027"

/note="Vector: TopoBlunt"

Alignment Scores:

Pred. No.: 6.27e+03

Score: 27.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Length: 285

Matches: 6

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-014-101B-41 (1-6) x CD152034 (1-285)

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CB921222 (1-279)

QY 1 IleThrArgAlaArgIle 6
Db 95 ATTACAAGACGCGGATA 78

RESULT 36

CD152034

LOCUS

DEFINITION

ML1-0027T-D047-H07-U.G ML1-0027 Schistosoma mansoni CDNA clone

ML1-0027T-D047-H07.G, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 285)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,

Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,

Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,

Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,

Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,

Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,

Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,

Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,

Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acoelomate human parasite Schistosoma

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Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquimica

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Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjo@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST

Genome Project. All sequences in the project were assembled and

annotated. This entry and all the assembled sequences can be seen

in the following URL http://bioinfo.iq.usp.br/schisto/

Plate: ML1-0027T-D047 row: 7 column: H.

Location/Qualifiers

1. .285

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="ML1-0027T-D047-H07.G"

/sex="mixed pool"

/dev_stage="miracidium"

/clone_lib="ML1-0027"

/note="Vector: TopoBlunt"

Alignment Scores:

Pred. No.: 6.27e+03

Score: 27.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Length: 285

Matches: 6

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-014-101B-41 (1-6) x CD152034 (1-285)

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CB921222 (1-279)

QY 1 IleThrArgAlaArgIle 6
Db 95 ATTACAAGACGCGGATA 78

RESULT 36

CD152034

LOCUS

DEFINITION

ML1-0027T-D047-H07-U.G ML1-0027 Schistosoma mansoni CDNA clone

ML1-0027T-D047-H07.G, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 285)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,

Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,

Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,

Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,

Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,

Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,

Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,

Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,

Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acoelomate human parasite Schistosoma

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Nat. Genet. 35 (2), 148-157 (2003)

22879926

12973350

Contact: Dr. Sergio Verjovski-Almeida

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Brasil

Tel: +55-11-3091-2173

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Email: verjo@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST

Genome Project. All sequences in the project were assembled and

annotated. This entry and all the assembled sequences can be seen

in the following URL http://bioinfo.iq.usp.br/schisto/

Plate: ML1-0027T-D047 row: 7 column: H.

Location/Qualifiers

1. .285

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="ML1-0027T-D047-H07.G"

/sex="mixed pool"

/dev_stage="miracidium"

/clone_lib="ML1-0027"

/note="Vector: TopoBlunt"

Alignment Scores:

Pred. No.: 6.27e+03

Score: 27.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Length: 285

Matches: 6

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-014-101B-41 (1-6) x CD152034 (1-285)

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101B-41 (1-6) x CB921222 (1-279)

QY 1 IleThrArgAlaArgIle 6
Db 95 ATTACAAGACGCGGATA 78

RESULT 36

CD152034

LOCUS

DEFINITION

ML1-0027T-D047-H07-U.G ML1-0027 Schistosoma mansoni CDNA clone

ML1-0027T-D047-H07.G, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 285)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,

Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,

Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,

Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,

Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,

Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,

Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,

Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,

Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acoelomate human parasite Schistosoma

mansoni

Nat. Genet. 35 (2), 148-157 (2003)

22879926

12973350

Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquimica

Instituto de Quimica - Universidade de Sao Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjo@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST

Genome Project. All sequences in the project were assembled and

annotated. This entry and all the assembled sequences can be seen

in the following URL http://bioinfo.iq.usp.br/schisto/

Plate: ML1-0027T-D047 row: 7 column: H.

Location/Qualifiers

1. .285

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

RESULT 40
BM348722/c
LOCUS
DEFINITION
sequence.
ACCESSION
BM348722
VERSION
BM348722.1 GI:18173334
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 289)
Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
Unpublished (2001)
JOURNAL
COMMENT
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
Phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
source
1. .289
/organism="Zea mays"
/mol_type="mRNA"
/cultiivar="B73"
/db_xref="taxon:4577"
/clone="MEST299-G08"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="ISUM5-RN"
/note="Vector: pT7T3PAC; Site 1: EcoRI; Site 2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65
DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear
(0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk,
unpollinated first ear, ear shank, etiolated seedlings,
callus, Cycloheximide-treated callus, Anaerobic treated
seedlings, NAA (a-Naphthalene acetic acid)-treated
seedlings, Kinetin-treated seedlings, ACPG
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscissic
acid)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
AACTGGAGCATTCGGCGCGAGGATTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the

ORIGIN
Alignment Scores:
Pred. No.: 6.36e+03 Length: 289
Score: 27.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-014-101B-41 (1-6) x BM348722 (1-289)
Qy 1 IleThrArgAlaArgile 6
Db 136 ATTACACGTGCACGCATT 119
Search completed: February 18, 2005, 07:01:04
Job time : 713.52 secs

EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."